



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 182280

TO: Phuong Bui
Location: REM/2A15/2C18
Art Unit: 1638
Friday, March 17, 2006
Case Serial Number: 10/634548

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518


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Search Notes

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PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
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PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
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PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
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PR 26-OCT-1999; 99US-0161361P.
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Query Match 96.2%; Score 1049; DB 3; Length 1088;
Best Local Similarity 98.8%; Pred. No. 1.3e-304;
Matches 1078; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

QY 1 AAAAAAAAAAATTAACAATAATCATTTCTTATCTTATGACTTGTCAAGATTCTCT 60
 Db 1 AAAAAAAAAAATTAACAATAATCATTTCTTATCTTATGACTTGTCAAGATTCTCT 60
 QY 61 TCTTCTTCTTCTTCT 120
 Db 61 TCTTCTTCTTCTTCT 120
 QY 121 TACCTCATCTCCGATCAATCATCAGTGTGTCGGATCGGGAACAACCTTTGACGATC 180
 Db 121 TACCTCATCTCCGATCAATCATCAGTGTGTCGGATCGGGAACAACCTTTGACGATC 180
 QY 181 ACCGGTCTGTCT 240
 Db 181 ACCGGTCTGTCT 240
 QY 241 TGGGCTCTGCTACTCAAGTACAGTGTGTCGGATCTCTGATCTTTCAGCAGTTCGACGA 300
 Db 241 TGGGCTCTGCTACTCAAGTACAGTGTGTCGGATCTCTGATCTTTCAGCAGTTCGACGA 300
 QY 301 ATTGCTGTGTCATGAGTCCGAGACACCGTGGACGCTTGTGGAGCATACCGGCTTG 360
 Db 301 ATTGCTGTGTCATGAGTCCGAGACACCGTGGACGCTTGTGGAGCATACCGGCTTG 360
 QY 361 TCTTAAGCTTCGAGAGTCTCAACAAGCGAAAGTCAATTCACAGAGTTTGAACAAGC 420
 Db 361 TCTTAAGCTTCGAGAGTCTCAACAAGCGAAAGTCAATTCACAGAGTTTGAACAAGC 420
 QY 421 TTGTGCTATATCTCTCAGGTCGTCTTTGCTGATCTTGTGCTGCGCAATCTTCAGCGAGTCGA 480
 Db 421 TTGTGCTATATCTCTCAGGTCGTCTTTGCTGATCTTGTGCTGCGCAATCTTCAGCGAGTCGA 480
 QY 481 CCGAGGCTCGATPACTTGTCTCTTCTTGTTCGTTAGTAAAGGCTTAAAGGCTTAAATTA 540
 Db 481 CCGAGGCTCGATPACTTGTCTCTTCTTGTTCGTTAGTAAAGGCTTAAAGGCTTAAATTA 540
 QY 541 ACGGCTATCCATTTCCCAAAATTCGATCTAATCAATCCGTCACAAGAGAGGAGAG 600
 Db 541 ACGGCTATCCATTTCCCAAAATTCGATCTAATCAATCCGTCACAAGAGAGGAGAG 600
 QY 601 CAGAAAGTGTCTTAAAGTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 660
 Db 601 CAGAAAGTGTCTTAAAGTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 660
 QY 661 TCTTCTGAGAGAGTCTCTAATCGGTATGATCTGTTAGCAATGATGTTGTTGTTGTTGTTG 720
 Db 661 TCTTCTGAGAGAGTCTCTAATCGGTATGATCTGTTAGCAATGATGTTGTTGTTGTTGTTG 720
 QY 721 GAATAGCTGATATATATGGAAGTAAAGTGGGTCAACTAAGATACCTTACCAACCAAGAA 780
 Db 721 GAATAGCTGATATATATGGAAGTAAAGTGGGTCAACTAAGATACCTTACCAACCAAGAA 780
 QY 781 AGAGTTGGGCGAAGAGCATCTCCATGTTCACTTCGCTTCTTATCTCCATCCGATTTAC 840
 Db 781 AGAGTTGGGCGAAGAGCATCTCCATGTTCACTTCGCTTCTTATCTCCATCCGATTTAC 840
 QY 841 TTTACTATTAACAAGCTTGGGTAACCTTCAATGAATGGGAAACGACCTTGGAGAGAG 900
 Db 841 TTTACTATTAACAAGCTTGGGTAACCTTCAATGAATGGGAAACGACCTTGGAGAGAG 900
 QY 901 TAGCAATGTCTCAATGTGTCACAGGTAGTCAATCCATCAACCATCAACCATCAATTAG 960
 Db 901 TAGCAATGTCTCAATGTGTCACAGGTAGTCAATCCATCAACCATCAACCATCAATTAG 960
 QY 961 ACGACAAATTTTGGGTTCTCTGCTACTATTTTAACTGCTTATTTAAAGTTTGGATTTT 1020
 Db 961 ACGACAAATTTTGGGTTCTCTGCTACTATTTTAACTGCTTATTTAAAGTTTGGATTTT 1020
 QY 1021 AGATTAATCCCTCAATTAACGAAATGTATATAGATTTTAAAGATCCGACCTTA 1080
 Db 1021 AGATTAATCCCTCAATTAACGAAATGTATATAGATTTTAAAGATCCGACCTTA 1080
 QY 1077 AGATTAATCCCTCAATTAACGAAATGTATATAGATTTTAAAGATCCGACCTTA 1077

QY 1081 CAATGTTTCC 1091
 Db 1078 CAATGTTTCC 1088
 RESULT 3
 ADX46288
 ID ADX46288 standard; cDNA; 1015 BP.
 AC ADX46288;
 XX
 DT 21-APR-2005 (first entry)
 DE
 XX Plant full length insert polynucleotide seqid 21028.
 KM plant protectant; plant growth regulant; gene therapy; plant;
 KM recombinant DNA construct; physical array; plant breeding marker;
 KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KM extreme osmotic condition; pathogen tolerance; pest tolerance;
 KM growth rate; cell cycle pathway; disease resistance;
 KM galactomannan production; lignin production; plant growth regulator;
 KM yield; plant growth; plant development; seed oil; protein yield;
 KM protein content; gene; ss.
 XX
 OS Unidentified.
 XX
 PN US2004034888-A1.
 XX
 PD 19-FEB-2004.
 XX
 PF 28-APR-2003; 2003US-00425114.
 XX
 PR 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX
 PA (LIU/) LIU J.
 PA (ZHOV/) ZHOV Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABAS/) TABASKA J E.
 PA (CAOV/) CAO Y.
 XX
 PI Lin J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX
 DR WPI; 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 21028; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html; DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 CC
 SQ Sequence 1015 BP; 228 A; 245 C; 219 G; 323 T; 0 U; 0 Other;

Query Match 93.0%; Score 1015; DB 13; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 2,2e-294;
 Matches 1015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 134 GATCAATCATAGTGTGTGCGGTTCGGGACAACTCTTGACGACTCAGCGTTCTGTC 193
Db 61 GATCAATCATAGTGTGTGCGGTTCGGGACAACTCTTGACGACTCAGCGTTCTGTC 120
Qy 194 TCCGGGCTCTGATTTCTTCTCTGTTTATAGTGTGACCGGAATGGGCTCTGCTAC 253
Db 121 TCCGGGCTCTGATTTCTTCTCTGTTTATAGTGTGACCGGAATGGGCTCTGCTAC 180
Qy 254 TCAGTTAAGTGTGTGCTGCTCTGATCTCTTACAGAGTTGCGAGAAATTCGCTTGCA 313
Db 181 TCAGTTAAGTGTGTGCTGCTCTGATCTCTTACAGAGTTGCGAGAAATTCGCTTGCA 240
Qy 314 TGAAGTGGAGCCACCGTGGAGTGTGTGAGACATACCGCTTGTCTTAAAGCTTGA 373
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Qy 374 GAGTCTACCAAGGAAAGCGTCAATTCAGAGTTAGAGAGAAAGCTGTGCAATATCT 433
Db 301 GAGTCTACCAAGGAAAGCGTCAATTCAGAGTTAGAGAGAAAGCTGTGCAATATCT 360
Qy 434 CTCAGTCTGCTTTTCTGACTGTGCGTGGCAATCTTACGCGGATCGACCGAGGCTCGATA 493
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Qy 494 CTTTGTGCTTTTGTTCGTTAGTGAATGCTTAAAGCTTGTATTAACGCAATATCAT 553
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Db 481 TTCCCAAAATCGAATGCAATCAAAATCGTCAAAAGAGAGAGAGAGAGAGAGTGTCT 540
Qy 614 TAAAGTCTCTTGTCTTCAAGTCTTACGCTCTTCTTCTGCGGTTTCTTCTGAGAGA 673
Db 541 TAAAGTCTCTTGTCTTCAAGTCTTACGCTCTTCTTCTGCGGTTTCTTCTGAGAGA 600
Qy 674 GTCTCTATGCGATGATCTGTTAGCAATGATGTGTGCGATGGAATAGCTGATAT 733
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Qy 734 AATGGGACGTAAAGTTGGGTCAATTAAGTCTTAAACCAAGAAAGAGTTGGGACG 793
Db 661 AATGGGACGTAAAGTTGGGTCAATTAAGTCTTAAACCAAGAAAGAGTTGGGACG 720
Qy 794 AAGCATCTCATGTTTCACTCTGCGCTTCTTCACTCCATCTTACTTACTATCTC 853
Db 721 AAGCATCTCATGTTTCACTCTGCGCTTCTTCACTCCATCTTACTTACTATCTC 780
Qy 854 AAGCTTGGGTACCTTCAATGAACCTGGGAAACGACTTGCAGAGAGTGAAGATGCTC 913
Db 781 AAGCTTGGGTACCTTCAATGAACCTGGGAAACGACTTGCAGAGAGTGAAGATGCTC 840
Qy 914 AATGGTGGCAAGGTAGTGGAGTGGTACCAATCAACCAATTAAGAGCAATATTTTC 973
Db 841 AATGGTGGCAAGGTAGTGGAGTGGTACCAATCAACCAATTAAGAGCAATATTTTC 900
Qy 974 GGTTCCTCTGCTATATTTAGTGTGTTTAAAGTTAGTATTAATATCCCTC 1033
Db 901 GGTTCCTCTGCTATATTTAGTGTGTTTAAAGTTAGTATTAATATCCCTC 960
Qy 1034 AATAACCGAATGTGTATATAGTATTTTAAAGATTCGACCTTACAAATGTT 1088
Db 961 AATAACCGAATGTGTATATAGTATTTTAAAGATTCGACCTTACAAATGTT 1015

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RESULT 4
 ADX31786
 ID ADX31786 standard; cDNA; 980 BP.
 XX
 AC ADX31786;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polynucleotide seqid 14606.
 XX
 XX plant protectant; plant growth regulator; gene therapy; plant;
 KM recombinant DNA construct; physical array; plant breeding marker;
 KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KM extreme osmotic condition; pathogen tolerance; pest tolerance;
 KM growth rate; cell cycle pathway; disease resistance;
 KM galactomannan production; lignin production; plant growth regulator;
 KM yield; plant growth; plant development; seed oil; protein yield;
 KM protein content; gene; ss.
 XX
 OS Unidentified.
 XX
 PN US2004034888-A1.
 XX
 PD 19-FEB-2004.
 XX
 PF 28-APR-2003; 2003US-00425114.
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 PR 06-MAY-1999; 99US-00304517.
 XX
 PR 05-NOV-2001; 2001US-00985678.
 XX
 PA (LITUJ/) LIU J.
 PA (ZHOUL/) ZHOU Y.
 PA (KOVAN/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABAS/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX
 DR WPI; 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 14606; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp://seqdata.uspto.gov/sequence.html; DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 CC
 SQ Sequence 980 BP; 223 A; 229 C; 215 G; 313 T; 0 U; 0 Other;

Query Match 89.6%; Score 977; DB 13; Length 980;
 Best Local Similarity 100.0%; Pred. No. 5.8e-283;
 Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 115 CAACCTTACCTCTATCTCCGATCATCATAGTGTGCGGTCGGGAAACAACCTTTGA 174
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Oy 235 CCGGAATGGGCTCTGCTACTGATTAAGTGTGCGGTCCTCTGATCTTCAAGCTT 294
Db 121 CCGGAATGGGCTCTGCTACTGATTAAGTGTGCGGTCCTCTGATCTTCAAGCTT 180
Oy 295 CGAGCAATTCGCTGTGATGACGTGCGAGCCACGTCGAGCTTGTGAGCAATACG 354
Db 181 CGAGCAATTCGCTGTGATGACGTGCGAGCCACGTCGAGCTTGTGAGCAATACG 240
Oy 355 CGCTTGTCTTAAGCTTGAAGTCTCACCAAGCGAAAGCTCATTCACAGTTGACA 414
Db 241 CGCTTGTCTTAAGCTTGAAGTCTCACCAAGCGAAAGCTCATTCACAGTTGACA 300
Oy 415 GAAAGCTTGTGATATCTCAGGTCGCTTCTGATCTTGTGCGGTCATCTTCAAGG 474
Db 301 GAAAGCTTGTGATATCTCAGGTCGCTTCTGATCTTGTGCGGTCATCTTCAAGG 360
Oy 475 GATGACCGAGGCTCGATCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 534
Db 361 GATGACCGAGGCTCGATCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 420
Oy 535 TTATTAACGACATTCATTTCCCAAAATTCGATGCTAATCCGTCACAGAGAG 594
Db 421 TTATTAACGACATTCATTTCCCAAAATTCGATGCTAATCCGTCACAGAGAG 480
Oy 595 GGAGAGAGAGAGTGTCTTAAAGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 654
Db 481 GGAGAGAGAGAGTGTCTTAAAGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 540
Oy 655 CGGTTTTCTTGTGAGAGAGTCTCTATCGGTAATCTCTGTAAGCAATGATGTGTG 714
Db 541 CGGTTTTCTTGTGAGAGAGTCTCTATCGGTAATCTCTGTAAGCAATGATGTGTG 600
Oy 715 GCGATGGAATGCTGATTTAATGGAGCTAAGTTGGGTCACTAAGTACCTTACAAC 774
Db 601 GCGATGGAATGCTGATTTAATGGAGCTAAGTTGGGTCACTAAGTACCTTACAAC 660
Oy 775 CAAGAAAGAGTGTGGGAGAGAGATCTGCATGCTTCTGAGCTTCTTCAATCCATCG 834
Db 661 CAAGAAAGAGTGTGGGAGAGAGATCTGCATGCTTCTGAGCTTCTTCAATCCATCG 720
Oy 835 CATTACTTATCTATTACTCAAGCTTGGGTACTTCAATGAACTGGGAAAGCACTTGC 894
Db 721 CATTACTTATCTATTACTCAAGCTTGGGTACTTCAATGAACTGGGAAAGCACTTGC 780
Oy 895 AGAGATGAGCAATGCTCAATGCTGCGCAGGTAAGTGAAGTCCGATCCATCCATC 954
Db 781 AGAGATGAGCAATGCTCAATGCTGCGCAGGTAAGTGAAGTCCGATCCATCCATC 840
Oy 955 AATTAGAGCAATATTCGGTCTCTGAGTCAATTTTATGCTTATTTATTAAGTTTGG 1014
Db 841 AATTAGAGCAATATTCGGTCTCTGAGTCAATTTTATGCTTATTTATTAAGTTTGG 900
Oy 1015 GATATTAGATTATTCCTCATTAACCGAATGTAATAGATTTTATTAAGATCCG 1074
Db 901 GATATTAGATTATTCCTCATTAACCGAATGTAATAGATTTTATTAAGATCCG 960
Oy 1075 ACCTTAACAATGTTCC 1091
Db 961 ACCTTAACAATGTTCC 977

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RESULT 5
ADXS4389
ID ADXS4389 standard; cDNA; 1062 BP.

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XX AC ADXS4389;
XX XX
XX 21-Apr-2005 (first entry)
XX DE Plant full length insert polynucleotide seqid 29129.
XX XX
XX plant protectant; plant growth regulant; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactomannan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.
XX OS Unidentified.
XX XX
XX US2004034888-A1.
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XX 19-FEB-2004.
XX XX
XX 28-APR-2003; 2003US-00425114.
XX PR 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.
XX XX
XX (LIU/) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABAS/) TABASKA J E.
XX (CAO/) CAO Y.
XX XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX DR WPI; 2004-180133/17.
XX XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX PT
XX XX
XX Claim 1; SEQ ID NO 29129; 15bp; English.
XX XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html; DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photoynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This sequence represents a plant full length insert
XX polynucleotide that can be used in the recombinant DNA construct of the
XX invention.
XX XX
SQ Sequence 1062 BP; 235 A; 264 C; 243 G; 320 T; 0 U; 0 Other;
Query Match 62.2%; Score 678.6; DB 13; Length 1062;
Best Local Similarity 82.6%; Pred. No. 3.8e-193;
Matches 777; Conservative 0; Mismatches 164; Indels 0; Gaps 0;
Oy 108 ATGGCAGCAACCTTACCTCTATCTCCGATCATCATAGTGTGCGGTCGGGAAACAAC 167
Db 46 ATGGCAGCAACCTTACCTCTATCTCCGATCATCATAGTGTGCGGTCGGGAAACAACG 105

```

KW	protein identification; signal transduction pathway; metabolic; pathway
KV	promoter; termination sequence; corn; ss.
XX	
OS	zea mays subsp. mays.
XX	
EN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-00301439.
XX	
FR	25-FEB-1999; 99US-0121825P.
FR	05-MAR-1999; 99US-0123180P.
FR	09-MAR-1999; 99US-0123548P.
PR	23-MAR-1999; 99US-0125788P.
PR	25-MAR-1999; 99US-0126264P.
PR	29-MAR-1999; 99US-0126785P.
PR	01-APR-1999; 99US-0127452P.
PR	06-APR-1999; 99US-0128234P.
PR	08-APR-1999; 99US-0128714P.
PR	16-APR-1999; 99US-0129845P.
PR	19-APR-1999; 99US-0130077P.
PR	21-APR-1999; 99US-0130449P.
PR	23-APR-1999; 99US-0130510P.
PR	28-APR-1999; 99US-0130891P.
PR	30-APR-1999; 99US-0132048P.
PR	04-MAY-1999; 99US-0132407P.
PR	05-MAY-1999; 99US-0132484P.
PR	06-MAY-1999; 99US-0132485P.
PR	06-MAY-1999; 99US-0132486P.
PR	07-MAY-1999; 99US-0132487P.
PR	11-MAY-1999; 99US-0132863P.
PR	14-MAY-1999; 99US-0134218P.
PR	14-MAY-1999; 99US-0134219P.
PR	14-MAY-1999; 99US-0134221P.
PR	14-MAY-1999; 99US-0134370P.
PR	18-MAY-1999; 99US-0134768P.
PR	19-MAY-1999; 99US-0134941P.
PR	20-MAY-1999; 99US-0135124P.
PR	21-MAY-1999; 99US-0135353P.
PR	24-MAY-1999; 99US-0135629P.
PR	25-MAY-1999; 99US-0136021P.
PR	27-MAY-1999; 99US-0136332P.
PR	28-MAY-1999; 99US-0136782P.
PR	01-JUN-1999; 99US-0137222P.
PR	03-JUN-1999; 99US-0137528P.
PR	04-JUN-1999; 99US-0137502P.
PR	07-JUN-1999; 99US-0137724P.
PR	08-JUN-1999; 99US-0138094P.
PR	10-JUN-1999; 99US-0138540P.
PR	10-JUN-1999; 99US-0138847P.
PR	14-JUN-1999; 99US-0139119P.
PR	16-JUN-1999; 99US-0139452P.
PR	16-JUN-1999; 99US-0139453P.
PR	17-JUN-1999; 99US-0139492P.
PR	18-JUN-1999; 99US-0139454P.
PR	18-JUN-1999; 99US-0139455P.
PR	18-JUN-1999; 99US-0139456P.
PR	18-JUN-1999; 99US-0139457P.
PR	18-JUN-1999; 99US-0139458P.
PR	18-JUN-1999; 99US-0139459P.
PR	18-JUN-1999; 99US-0139460P.
PR	18-JUN-1999; 99US-0139461P.
PR	18-JUN-1999; 99US-0139462P.
PR	18-JUN-1999; 99US-0139463P.
PR	18-JUN-1999; 99US-0139750P.
PR	21-JUN-1999; 99US-0139763P.
PR	22-JUN-1999; 99US-0139817P.
PR	22-JUN-1999; 99US-0139889P.
PR	23-JUN-1999; 99US-0140033P.
PR	23-JUN-1999; 99US-01400354P.

PR	26-JUN-1999	99US-01406595P
PR	26-JUN-1999	99US-01406921P
PR	29-JUN-1999	99US-01409319P
PR	30-JUN-1999	99US-0141827P
PR	01-JUL-1999	99US-0141642P
PR	01-JUL-1999	99US-0142154P
PR	02-JUL-1999	99US-0142055P
PR	06-JUL-1999	99US-0142390P
PR	08-JUL-1999	99US-0142803P
PR	09-JUL-1999	99US-0142202P
PR	13-JUL-1999	99US-0143297P
PR	13-JUL-1999	99US-0143342P
PR	14-JUL-1999	99US-0143624P
PR	15-JUL-1999	99US-0144005P
PR	16-JUL-1999	99US-0144086P
PR	16-JUL-1999	99US-0144335P
PR	19-JUL-1999	99US-0144343P
PR	20-JUL-1999	99US-0144352P
PR	20-JUL-1999	99US-0144362P
PR	20-JUL-1999	99US-0144684P
PR	21-JUL-1999	99US-0144431P
PR	21-JUL-1999	99US-0144481P
PR	21-JUL-1999	99US-0144508P
PR	21-JUL-1999	99US-0145088P
PR	22-JUL-1999	99US-0145087P
PR	22-JUL-1999	99US-0145087P
PR	22-JUL-1999	99US-0145089P
PR	22-JUL-1999	99US-0145192P
PR	23-JUL-1999	99US-0145145P
PR	23-JUL-1999	99US-0145218P
PR	23-JUL-1999	99US-0145224P
PR	26-JUL-1999	99US-0145376P
PR	27-JUL-1999	99US-0145513P
PR	27-JUL-1999	99US-0145518P
PR	27-JUL-1999	99US-0145519P
PR	04-AUG-1999	99US-0145519P
PR	05-AUG-1999	99US-0145911P
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PR	02-AUG-1999	99US-0146388P
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PR	09-AUG-1999	99US-0148171P
PR	11-AUG-1999	99US-0148319P
PR	12-AUG-1999	99US-0148341P
PR	13-AUG-1999	99US-0148565P
PR	13-AUG-1999	99US-0148684P
PR	16-AUG-1999	99US-0149368P
PR	17-AUG-1999	99US-0149375P
PR	18-AUG-1999	99US-0149426P
PR	20-AUG-1999	99US-0149723P
PR	20-AUG-1999	99US-0149929P
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PR	27-AUG-1999	99US-0151066P
PR	30-AUG-1999	99US-0151080P
PR	31-AUG-1999	99US-0151303P
PR	01-SEP-1999	99US-0151930P

PR	17.-SEB-1399	99US-0153263P
PR	10.-SEB-1399	99US-0153070P
PR	13.-SEB-1399	99US-0153758P
PR	15.-SEB-1399	99US-0154018P
PR	16.-SEB-1399	99US-0154039P
PR	20.-SEB-1399	99US-0154777P
PR	22.-SEB-1399	99US-0155133P
PR	23.-SEB-1399	99US-0155586P
PR	24.-SEB-1399	99US-0155658P
PR	26.-SEB-1399	99US-0156458P
PR	29.-SEB-1399	99US-0156569P
PR	04.-OCT-1399	99US-0157117P
PR	05.-OCT-1399	99US-0157753P
PR	06.-OCT-1399	99US-0157865P
PR	07.-OCT-1399	99US-0158029P
PR	08.-OCT-1399	99US-0158932P
PR	12.-OCT-1399	99US-0158369P
PR	13.-OCT-1399	99US-0159294P
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PR	18.-OCT-1399	99US-0159568P
PR	21.-OCT-1399	99US-0160741P
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PR	25.-OCT-1399	99US-0161404P
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PR	26.-OCT-1399	99US-0161539P
PR	26.-OCT-1399	99US-0161560P
PR	26.-OCT-1399	99US-0161361P
PR	28.-OCT-1399	99US-0161920P
PR	28.-OCT-1399	99US-0161922P
PR	28.-OCT-1399	99US-0161939P
PR	29.-OCT-1399	99US-0162142P

Query Match	45.2%	Score 492.8;	DB 3;	Length 494;
Best Local Similarity	99.4%	Pred. No. 2.1e-137;		
Matches 491; Conservative	3;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	AAAAAAGATTAATATGACAAAATATCATTTTCCCTATATCTATATGACATGACAGATCTCT	60
QY	1	AAAAAAGATTAATATGACAAAATATCATTTTCCCTATATCTATATGACATGACAGATCTCT	60
QY	1	AAAAAAGATTAATATGACAAAATATCATTTTCCCTATATCTATATGACATGACAGATCTCT	60
QY	61	TCTTCTTCTTCTTCTCTCTCTCTCCCAACTCAGTTCCTCCCTGCATAGGACGAACCT	120
QY	61	TCTTCTTCTTCTTCTCTCTCTCTCCCAACTCAGTTCCTCCCTGCATAGGACGAACCT	120
QY	121	TACCTCTATCTCCGATCAATCATCATGTTGTGTGCGGTGCGGAACAACCTTTTACGACATC	180
QY	121	TACCTCTATCTCCGATCAATCATCATGTTGTGTGCGGTGCGGAACAACCTTTTACGACATC	180
QY	181	ACCGGTTCTGTCTCTCGGCTTCTTGATTTCTTCTCTTGTGTTTCAATGGTTGACCGGAA	240
QY	181	ACCGGTTCTGTCTCTCGGCTTCTTGATTTCTTCTCTTGTGTTTCAATGGTTGACCGGAA	240
QY	241	TGGGCTCTGCTACTAGTTACGTCGTCGTCGTCCTCTCTGATCTCTTACGAGATGCGACGA	300
QY	241	TGGGCTCTGCTACTAGTTACGTCGTCGTCGTCCTCTCTGATCTCTTACGAGATGCGACGA	300
QY	301	ATTGCTCTTGATGATACGTCGGAAGCAACCGTGGACAGTCTTGATGAGCATACACGCTTG	360
QY	301	ATTGCTCTTGATGATACGTCGGAAGCAACCGTGGACAGTCTTGATGAGCATACACGCTTG	360

DB 61 TCTTCTTTCTTCCTCCCTCCCAACTCAGTTCCTTCCGTCCATGCGACGAACCT 120

CC <http://seqdata.uspto.gov/sequence.html?docid:2004034888>. The polynucleotide

of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the invention.

Sequence 1007 BP, 208 A; 248 C; 186 G; 365 T; 0 U; 0 Other;

Query Match 30.9%; Score 337; DB 13; Length 1007;

Best Local Similarity 64.3%; Pred. No. 2.3e-90;

Matches 505; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

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Oy 280 TCTCTTACGAGTTGCGCGAATTCGCTTGATGACGTGGAGCCCGGTGGACATGC 339
    |||
Db 181 TCTCAGCCACCGCTGTACCGCTCTATCTCCGAGATACCGCTGCTTGGCT 240
    |||
Oy 340 TTGGTGAGCATACGCGCTTGTCTTAAGCTTCGAGAGTCTCAACCAAGCAACGTCATTC 399
    |||
Db 241 TTGCTGGCGCTTATGCTCTGCTTCACTTGATTTCTCACTCAAAAGAGCTCATTC 300
    |||
Oy 400 AACGAGTTTGAGCAGAAAGCTTGTGATATATCTCAAGTCTGCTTTTCTACTTGGCT 459
    |||
Db 301 AGCAGAAATTTAAGTGAATAATGGTGATATATATCTGAGATTACTTTTGGCAATTTCT 360
    |||
Oy 460 GGCCTAATCTTCAAGCGGATGACCGGAGCTGATCTTGTGCTTTTCTTCCGTAGCA 519
    |||
Db 361 GGCCTAATTTGACGACCGGAGTGAAGCTGCTGATCTTGTGATCTGCTTCACTTTCA 420
    |||
Oy 520 ATGGCTTAAGCTTGTATTAACGAGATATCCCAATTCGATGCTATCAAT 579
    |||
Db 421 ATTGCTTAAGCTTGTATTAATGATGCTCTCTTTGACGATGATCAAGCTTGAATCAAT 480
    |||
Oy 580 CCGTCAAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 639
    |||
Db 481 CTGTTACTCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
    |||
Oy 640 CTCTCTTTCTCTGCGGTTTCTCTGAGAGAGATCTTCTGATGATGATCTGTTAG 699
    |||
Db 541 TGTGATGTTATGTCCTCTGTTGTTGGCGGAAATCCCCGCTGGGTGATCTGCTGG 600
    |||
Oy 700 CAATGATGTTGATGCGGATGAGATGATGATATATGAGAGAGAGAGAGAGAGAGAGAG 759
    |||
Db 601 CAATGATGTTGCGGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
    |||
Oy 760 AGATACCTTTACACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 819
    |||
Db 661 AGATACCTTTATATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
    |||
Oy 820 TCTTATGCTTCAATGCTTCAATGCTTCAATGCTTCAATGCTTCAATGCTTCAATGCT 879
    |||
Db 721 TCAATATTTCTTATGCTTCAATGCTTCAATGCTTCAATGCTTCAATGCTTCAATGCT 780
    |||
Oy 880 GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 939
    |||
Db 781 GGGAGATATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
    |||
Oy 940 TACCATCATCGATCAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 999
    |||
Db 841 TTCCATATTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
    |||
Oy 1000 CTATTTAAGTTTGGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1059
    |||
Db 901 CCTATTTAAGTTTGGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
    |||

```

Oy 1060 TTTT 1064
 |||
 Db 961 TTCTT 965

RESULT 9

ID ADX51853 standard; cDNA; 1033 BP.

XX ADX51853;

XX 21-APR-2005 (first entry)

DE Plant full length insert polynucleotide seqid 26593.

KW plant protectant; plant growth regulator; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.

XX Unidentified.

OS US200403488-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LNU//) LNU J.

XX (ZHO//) ZHO Y.

XX (KOVA//) KOVALIC D K.

XX (SCRE//) SCREEN S E.

XX (TAB//) TABASKA J E.

XX (CAO//) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

PT New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.

PS Claim 1; SEQ ID NO 26593; 15pp; English.

CC The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at <http://seqdata.uspto.gov/sequence.html?docID:200403488>. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the invention.

XX Sequence 1033 BP, 170 A; 287 C; 282 G; 294 T; 0 U; 0 Other;

Query Match 27.0%; Score 294.6; DB 13; Length 1033;
 Best Local Similarity 62.9%; Pred. No. 1.3e-77;
 Matches 456; Conservative 0; Mismatches 269; Indels 0; Gaps 0;

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QY 294 GCGAGCAATTGCTGTCATGACGTCGAGCCACCGTGGAGTGTGTCGAGCATAC 353
    |||||
DB 192 GCGAGCCCGGGGGGGGCGGGAATGCGCGCGCATGTCATACCGCGGGGCGGTAC 251
    |||||
QY 354 GCGCTGTCTTAAGCTTGAAGTCTCAACGAGAAAGTCATTCACAGAGTTTGAAC 413
    |||||
DB 252 TCCCTGGCGCGCTTCGACGCGGCTCAAGCGCGCTCATCGAACAGAACTGAGC 311
    |||||
QY 414 AGAAGCTTGTGATATATCTCTCAGTGTGCTTTGCTGACTTGGTGGCCAACTTTCAGC 473
    |||||
DB 312 AGAATAATTGTGATGTCCTCTCCGAGTCCGTTCATGCTTCTTGGCCACTATTAAGT 371
    |||||
QY 474 GGATCGACCGAGGCTCGATTAATCTTGTCTTTGTTCCGTTAGTGAATGCTTAAAGCTT 533
    |||||
DB 372 AATTGACAGAAAGCAGGTTCTTGGCGCAATGTCCGTTGTGTAATCGATTAAGGCTT 431
    |||||
QY 534 GTTATTAAGCACTATTCATTTCCCAATTGATGCTTAATCAATCCGTCAAGAGAA 593
    |||||
DB 432 CTGACCTACGGGCTCCGCTTCCACTGATGAAGCTAGTAAATCGGTGACCGGTGAA 491
    |||||
QY 594 GGGAGAGAGAAAGTTGCTTAAAGTCTTGTGCTAGTCTTCTTCTTCTTCTTCT 653
    |||||
DB 492 GGAATAACAGAGAAATGTCTAGAGTCTCTGTAATGTAATGTCCTCTGTCAGT 551
    |||||
QY 654 GCGCTTTCTTCTGAGAGAGTCTCTTATCGGTATGATCTGTTAGCAATGATGTGAT 713
    |||||
DB 552 GTTTTGGCTTCTGCGCGCAATCTCTATTTGGGANTGTTTGTGTGATGATAGTGTGT 611
    |||||
QY 714 GCGATGCAATGCTGATATTAATGAGCACTTAAGTTGGGTCACTAAGATACCTTAAC 773
    |||||
DB 612 GGTATGCTTGTGCTGACATTTGTTGGGAGAAAGTATGCTCCGCAAGCTCCATTTCAAT 671
    |||||
QY 774 CCAAGAAAGATTTGGGAGAGAAATCTCAATGTTCACTTCCGCTTTTCATCTCCATC 833
    |||||
DB 672 GAGAACAGAGCTGATATGAAAGCACTCAATGTTCAATTTCTGCTTCTTCTATCTGCA 731
    |||||
QY 834 GCATTAATTTACTTACTTCAAGCTTGGGTGATCACTTCAATGAATGGGAAACGACTTG 893
    |||||
DB 732 CTGATGCTTCTTCTTCTTCTGCTTGTGTTACTTCACTGCTCTGTGGGATCTGGCAATT 791
    |||||
QY 894 CAGAGAGTGAAGTCTCAATGCTGCCACGAGTGTGAGTGTGCTTCAATCAATCCGAT 953
    |||||
DB 792 GGTAAACTGCTCTTGTGATTAAGCACTGTAAGTGTGATTTCTGTCAATGAT 851
    |||||
QY 954 CAATTAAGCAATATTTGCTTCTGCTACTATTTAGCTTATTTAAGTTTC 1013
    |||||
DB 852 GTTGTGATTAATCTCTGCTTCTTGTGCTTGTGCTTGTGCTTGTATTT 911
    |||||
QY 1014 GGATA 1018
    |||||
DB 912 GGCTA 916
    |||||

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RESULT 10
 ADX47586
 ID ADX47586 standard; cDNA; 1085 BP.

XX ADX47586;

XX 21-APR-2005 (first entry)

XX Plant full length insert polynucleotide seqid 22326.

XX plant protectant; plant growth regulant; gene therapy; plant;
 KM recombinant DNA construct; physical array; plant breeding marker;
 KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KM extreme osmotic condition; pathogen tolerance; pest tolerance;
 KM growth rate; cell cycle pathway; disease resistance;

KM galactomannan production; lignin production; plant growth regulator;
 KM yield; plant growth; plant development; seed oil; protein yield;
 KM protein content; gene; ss.

OS unidentified.

XX US200403488-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIU/J) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVA/) KOVALIC D K.

XX (SCRE/) SCREEN S E.

XX (TABAS/) TABASKA J E.

XX (CAO/Y) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to

XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or

XX pests, for conferring increased resistance to plant disease, or for

XX improving yield.

XX Claim 1; SEQ ID NO 22326; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a

XX polynucleotide consisting of a sequence encoding an amino acid sequence

XX available in electronic form from the US patent office at

XX ftp://seqdata.uspto.gov/sequence.html?docid:200403488. The polynucleotide

XX of the invention are also useful in physical arrays of molecules and as

XX plant breeding markers. The recombinant DNA construct is useful for

XX improving plant tolerance to cold, heat, drought, herbicides, extreme

XX osmotic conditions, pathogens or pests, for manipulating growth rate in

XX plant cells by modification of the cell cycle pathway, for conferring

XX increased resistance to plant disease, for producing galactomannan,

XX lignin or plant growth regulators, for increasing the rate of homologous

XX recombination in plants, for improving yield by modification of

XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

XX or by providing improved plant growth and development under at least one

XX stress condition or for modifying seed oil or protein yield and/or

XX content. This sequence represents a plant full length insert

XX polynucleotide that can be used in the recombinant DNA construct of the

XX invention.

XX Sequence 1085 BP; 178 A; 307 C; 298 G; 302 T; 0 U; 0 Other;

XX Query Match 27.0%; Score 294.6; DB 13; Length 1085;

XX Best Local Similarity 62.9%; Pred. No. 1.4e-77;

XX Matches 456; Conservative 0; Mismatches 269; Indels 0; Gaps 0;

```

QY 294 GCGAGCAATTGCTGTCATGACGTCGAGCCACCGTGGAGTGTGTCGAGCATAC 353
    |||||
DB 260 GCGAGCCCGGGGGGGGCGGGAATGCGCGCGCATGTCATACCGCGGGGCGGTAC 319
    |||||
QY 354 GCGCTGTCTTAAGCTTGAAGTCTCAACGAGAAAGTCATTCACAGAGTTTGAAC 413
    |||||
DB 320 TCCCTGGCGCGCTTCGACGCGGCTCAAGCGCGCTCATCGAACAGAACTGAGC 379
    |||||
QY 414 AGAAGCTTGTGATATATCTCTCAGTGTGCTTTGCTGACTTGGTGGCCAACTTTCAGC 473
    |||||
DB 380 AGAATAATTGTGATGTCCTCTCCGAGTCCGTTCATGCTTCTTGGCCACTATTAAGT 439
    |||||
QY 474 GGATCGACCGAGGCTCGATTAATCTTGTCTTTGTTCCGTTAGTGAATGCTTAAAGCTT 533
    |||||
DB 440 AATTGACAGAAAGCAGGTTCTTGGCGCAATGTCCGTTGTGTAATCGATTAAGGCTT 499
    |||||

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QY 534 GTTATTACGGAATCATCATTTCCCAAAATTCAGTGTATCAATCCGTACAGAGAA 593
DB 500 CTGACCTTAGGGGCTCCGCTTTCACTGATGAGCTCTAGTAAGTCCGTGACCCGTGAA 559
QY 594 GGGAGAGAGAGAGATTGCTTAAAGTCTTTGTTCTAAGTCTTCTTCTTCTCT 653
DB 560 GGAAGAACAGAGGATGCTGAGAGTCTCTGATCTATGTCATGTCCTGCTGGTCAGT 619
QY 654 GCGGTTTCTTCTGAGAGAGTCTCTATCGGTATGATCTGTTAGCAATGATGTGTGT 713
DB 620 GTTTTGGCTCTTGGCGGCGAGTCTCTAATGGAGATGTTTGTGTGATGATGATGTGT 679
QY 714 GGGCAGTGAATAGCTGATATATATGGAGGTAGTGGGTCAACTAAGATCCTTACAC 773
DB 680 GGTGATGCTTTGCTGACATTTGTTGGAGAAAGTATGCTCCGCAAGCTGCCATTCAT 739
QY 774 CCAAGAAAGAGTGGGAGAGAGCATCTCAATGTTCACTTCGCTTCTTCAATCTCCATC 833
DB 740 GAGAACAAAGACTGATAGAGAGATCTCAATGTTCAATTTCTGCTTCTTCTATCTGCA 799
QY 834 GCATTACTTACTATTAATCTCAAGCTTGGGTACCTTCAATGAACTGGGAAACGACCTTG 893
DB 800 CTGATGCTGTTCTACTTCTCTGCTTGTACTTCACTGTCCTGCTGGATCTGGCACTT 859
QY 894 CAGAGAGTGAAGAGTGTCTCAATGCTGCGCAAGGATGAGTGGCTACCCATCCAGAT 953
DB 860 GGTAACTGCTCTTGTGACATTAACACTACTGATAGAGAGTATTCCTGTCATATAT 919
QY 954 CAATTAGACGACATATATTCGGTCTCTGCTGCTACTATTTTAACTGCTTATTTAAGTTTC 1013
DB 920 GTTGTGATGACATATATCTCCGTTCTTGTGGCAATGTTGGCAGCTATCTGTATTT 979
QY 1014 GGATA 1018
DB 980 GGCTA 984

RESULT 11
ADX48515
ID ADX48515 standard; cDNA, 798 BP.
XX
AC ADX48515;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 23255.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
XX
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCREEN/) SCREEN S E.
PA (TABAS/) TABASKA J E.

```

```

PA (CAO/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JB, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 23255; 15pp; English.
XX
SS
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp://seqdata.uspto.gov/sequence.html/docid:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 798 BP; 159 A; 195 C; 223 G; 221 T; 0 U; 0 Other;

Query Match 26.5%; Score 289; DB 13; Length 798;
Best Local Similarity 62.6%; Pred. No. 5.7e-76;
Matches 451; Conservative 0; Mismatches 270; Indels 0; Gaps 0;

QY 286 CAGCAGTTGCGACCAATTCGCTGTTGCATGACGTGAGCAGCCGTGGCAGTGGCTG 345
DB 2 CGGCGCGGCGCCGCCAGCGGTGCTGAGAGCGAGCGTACATGTGCTATCACCGCG 61
QY 346 GAGCATACGCGCTGTGCTTAAAGCTTTCGAGAGTCTCACCAAGCAAACTCATTAACAGA 405
DB 62 GCGCTACTCTCTTGTGGCGCTTTCGACGAGCTCACCGAGCGGCGCTCATCGAAAGA 121
QY 406 GTTTGAGCAGAAAGCTTGTGATATCTCTAGGCTGCTTTGGTACTTGGCGCCAA 465
DB 122 GCTTGAAGCAGAAAGTGTGACAGTGTATCCGCGCTCTGTCAATGTATCTTGGCC 181
QY 466 TCTTCAGCGATTCGACGAGGCTGATCTTGTGCTGTTTGTTCGGTAAATGAGCT 525
DB 182 TGTTCAGCAATTCACAGACAGGATTTCCGCGGCTGTCCGTTCTGAACTCA 241
QY 526 TAAAGCTTGTATTAAGCACTATCATTTCCCAATTTGATGATCAATCAATCGTCA 585
DB 242 TGAAGCTTGTATTAAGCACTATCCGCTCTACAGTAAAGCTGTGTAATAATCAGTGA 301
QY 586 CAAGAGAGAGAGAGCAAGAGTTCCTTAAAGTCTTGTCTACGTTCTAGCTCTTC 645
DB 302 CACGTGAAGAGAAACCAAGAGAAATTCGAGAGGTCACCTGATATATCTCGGTGCTGC 361
QY 646 TTTTCTGCGGTTTCTTCTGAGAGAGTCTCTATCGGTATGATCTGTTAGCAATGA 705
DB 362 TGTTCAGGCTTTTATGCTCTTGGGATGATCCCATGAGGATGCTCTTGTGATGA 421
QY 706 TGTGTGTGGAGATGATAGCTGATATATATGAGAGTAAATTTGGTCAACTAAGATAC 765
DB 422 TGAAGGCTGAGAGGATTTTCTGACATTTGTTGAGAGGATATGAGCTCAAGGAAGCTGC 481
QY 766 CTTACACCCCAAGAAAGATTTGGGAGAGACATCTCATGTTTCTTGGCTTCTCA 825
DB 482 CATTCATTCGAGAGAGAGTGGCGCGGAGACATCTCATATTTCTGGTTCGTGC 541

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XX 19-FEB-2004.
 PD 28-APR-2003; 2003US-00425114.
 XX 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABAS/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 DR New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 PS Claim 1; SEQ ID NO 25671; 15pp; English.
 XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp://seqdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length yield
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 CC
 XX Sequence 723 BP; 145 A; 174 C; 198 G; 206 T; 0 U; 0 Other;
 SQ
 Query Match 25.2%; Score 274.8; DB 13; Length 723;
 Best Local Similarity 63.4%; Pred. No. 1e-71;
 Matches 420; Conservative 0; Mismatches 242; Indels 0; Gaps 0;

DB 307 CTGTTCAGCGTTTACGTTCTTTCGAGCGTAGGACCCCAATCGGAGATGCTCTGTGTCGATG 366
 QY 705 ATGTGTGGTGGCGAATGGAATGCTGATATTAATGGAGCTAAGTTTGGCTCACTAAGATA 764
 DB 367 ATGAGCGGTGGCGATGATGTTTGTGCTGACATTTGTGGAGAGATGCTGCGAAGCTG 426
 QY 765 CCTTACAAACCAAGAAAGTTGGGAGAGACATCTTCATGTTCACTTGGGCTTTC 824
 DB 427 CCATTCAATCGGAAGAGAGCTGGGCGGAGCATCTGATGTTTCACTTCTGTTCTG 486
 QY 825 ATCTTCATCGCATTAATTACTTAATCAAGCTTGGATCCTTCAATGAACTGGAA 884
 DB 487 CTGTCCGCGATGATGATGCTCTACTCTCAAGCTGGGTTACATGATGATGATGCGGAA 546
 QY 885 ACGACCTTGCAGAGATGACATGCTCTCATGATGATGCGGATGATGATGATGATGATG 944
 DB 547 GAGGCACTGGTGAAGCTGGCGCTTGTGACATTCACAGCAGATGAGTGGAGTGGCTCT 606
 QY 945 ATCAACGATCAATTAGACGACATATTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1004
 DB 607 GTGACCGAAGTTGATGATGACACATATCTTCTTGGCCACATGCTGATGCTTT 666
 QY 1005 TT 1006
 DB 667 CT 668
 XX
 XX RESULT 15
 XX ADX51758
 XX ID ADX51758 standard; cDNA; 753 BP.
 XX
 XX ADX51758;
 XX
 XX 21-APR-2005 (first entry)
 XX
 XX Plant full length insert polynucleotide seqid 26498.
 XX
 XX plant protectant; plant growth regulator; gene therapy; plant;
 XX recombinant DNA construct; physical array; plant breeding marker;
 XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 XX extreme osmotic condition; pathogen tolerance; pest tolerance;
 XX growth rate; cell cycle pathway; disease resistance;
 XX galactomannan production; lignin production; plant growth regulator;
 XX yield; plant growth; plant development; seed oil; protein yield;
 XX protein content; gene; ss.
 XX
 XX Unidentified.
 XX OS
 XX US200403488-A1.
 XX
 XX 19-FEB-2004.
 XX
 XX 28-APR-2003; 2003US-00425114.
 XX
 XX 06-MAY-1999; 99US-00304517.
 XX
 XX 05-NOV-2001; 2001US-00985678.
 XX
 XX (LIUJ/) LIU J.
 XX (ZHOU/) ZHOU Y.
 XX (KOVA/) KOVALIC D K.
 XX (SCRE/) SCREEN S E.
 XX (TABAS/) TABASKA J E.
 XX (CAOY/) CAO Y.
 XX
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 XX
 XX New recombinant DNA construct, useful for improving plant tolerance to
 XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 XX pests, for conferring increased resistance to plant disease, or for
 XX improving yield.

PS Claim 1; SEQ ID NO 26498; 15bp; English.
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp://seqdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 CC
 XX

SQ Sequence 753 BP; 154 A; 180 C; 206 G; 213 T; 0 U; 0 Other;

Query Match 25.2%; Score 274.8; DB 13; Length 753;
 Best Local Similarity 63.4%; Pred. No. 1e-71;
 Matches 420; Conservative 0; Mismatches 242; Indels 0; Gaps 0;

QY	345	GGAGCATCGCGCTTGTCTTAAGCTTCGAGAGTCTACCAAGCGAAGCATTCACAG	404
DB	16	GGCGCTTACTCTTGTGGCGCTTTCGACGAGCTCACGAGCGCGCTCATTCGAAAG	75
QY	405	AGTTGACGAGAAAGCTTGATGATTAAGCTTCAGGCTGCTTTTGTGTACTTGCGTGCCA	464
DB	76	AGCTTGACGAGAAAGGTTGTGACGCTGCTCGCGCTGCTGTTGATGATCTTGCGCC	135
QY	465	ATCTTACGGGATCGACCGAGGCTGATATCTTGCTGCTTTTGTTCGTTAGTGATGCG	524
DB	136	CTGTTACGCAATTCGACGAGACGACGATTTGCGCGGCTTCCCTTCGAACTCC	195
QY	525	TTAAGGCTTGTATTAAAGGACTATCAATTCGCCAATTCGATGCTAATCAATCCGTC	584
DB	196	ATGAGGCTTGTATATATGAGCTCCGCTCTACACTGATGAAGCTCTGTAATCAATG	255
QY	585	ACAGAGAAAGGAGAGACAGAGAGTGTCTTAAGGCTCTTGTCTTAAGCTCTT	644
DB	256	ACAAGTGAAGAAACAGAGAAATTTGCTGAGAGGTCACCTATATATGTCGTGCTG	315
QY	645	CTTTCTCTGCGGTTTCTTCTGAGAGAGTCTCCTATCGGTATGATCTCGTTAGCAATG	704
DB	316	CTGTTACAGCGTTTGTAGTCTTCTGCGGTGATGCCCATCGGAGATGCTCTCTTGTGATG	375
QY	705	ATGTTGTTGGCGAGTGAATAGCTGATATTAATGGAGAGTGAAGTTGGGCACTAAGATA	764
DB	376	ATGAGCGGTGGGAGTGGTTCCCTACATTTGTTGGAGAGAGTATGGCTCAGAGAGCTG	435
QY	765	CCTTACAAACCAAGAAAGTGTGGCAGAGACATCTCCATGTTCACTTCGCTTCTTC	824
DB	436	CCATTCAATCGAAGAGAGCTGGGCGGAGACATCTGATGTTTCTGTTTCCG	495
QY	825	ATCTTCATCGCACTTACTTACTTACTCAAGCTTTGGGTACTTCACTGAACCTGGAA	884
DB	496	CTGTCCGGAGTATGATGCTTACTTCTCAAGCTTGGGTTACATGATGTTATCTGGGAA	555
QY	885	ACGACCTTGACAGAGTAGCAATGGTCAATGATGCGCACGAGTGAAGTGGTACCC	944
DB	556	GAGGACCTTGTGTAAGTGGCGCTTGTGACCTAGACGACAGTATGAGTGGTCTCT	615
QY	945	ATCACCGATCAATTAAGACGACATATTTGCTTCTCTGCTACTATTTTACCTGCTAT	1004
DB	616	GTGACCGAAGTGTATGATGACAAACATATCTGTTCTTGGCCACCATGCTGTAGCTTT	675
QY	1005	TT 1006	

DB 676 CT 677

Search completed: March 16, 2006, 16:17:26
 Job time : 1194 secs

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OM protein - protein search, using sw model

Run on: March 16, 2006, 18:50:48 ; Search time 90 Seconds
(without alignments)

1484.124 Million cell updates/sec

Title: US-10-634-548-2

Perfect score: 1536
Sequence: 1 MAATLPSPINHQCRCFGNN.....DDNISVPLATIAAYLSFGY 304

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1536	100.0	304	8	ADJ98164 Thale cre
2	1536	100.0	315	8	ADJ91881 Plant ful
3	1523	99.2	301	8	ADJ91882 Plant ful
4	1523	99.2	304	3	AAG14596 Arabidops
5	1282	83.5	260	3	AAG14597 Arabidops
6	1266	82.4	304	8	ADJ98201 Rape phyt
7	1266	82.4	319	8	ADJ91966 Plant ful
8	1140	74.2	226	8	ADJ98166 Thale cre
9	870	56.6	306	8	ADJ91971 Plant ful
10	864	56.2	298	8	ADJ98203 Upland co
11	857.5	55.8	302	8	ADJ98207 Soybean p
12	791.5	51.5	314	8	ADJ98208 Rice phyt
13	791.5	51.5	312	8	ADJ98211 Plant ful
14	791.5	51.5	657	8	ADJ98211 Rice phyt
15	791.5	51.5	803	8	ADJ98210 Rice phyt
16	786	51.2	309	8	ADJ92772 Rice phyt
17	782.5	50.9	269	8	ADJ98209 Rice phyt
18	777	50.6	303	8	ADJ98223 Corn phyt
19	776	50.5	251	8	ADJ93203 Plant ful
20	773	50.3	300	8	ADJ98220 Bread whe
21	773	50.3	312	8	ADJ91977 Plant ful
22	752.5	49.0	267	8	ADJ98224 Corn phyt
23	751	48.9	233	8	ADJ91967 Plant ful
24	751	48.9	236	8	ADJ98225 Corn phyt

25	751	48.9	236	8	ADJ93050 Plant ful
26	718.5	46.8	292	8	ADJ98206 Soybean p
27	646	42.1	199	3	ADJ24830 Plant ful
28	643	41.9	129	3	AAG58667 Zea mays
29	615	40.0	191	8	ADJ98217 Sorghum p
30	607	39.5	259	8	ADJ58468 Plant pol
31	591	38.5	188	8	ADJ98222 Corn phyt
32	572.5	37.3	312	8	ADJ98227 Corn phyt
33	572.5	37.3	338	8	ADJ93092 Plant ful
34	565.5	36.8	246	8	ADJ98212 Rice phyt
35	562.5	36.6	302	8	ADJ98226 Bread whe
36	552.5	36.0	296	8	ADJ98218 Plant ful
37	552.5	36.0	296	8	ADJ91976 Plant ful
38	544	35.4	346	8	ADT60333 Plant pol
39	542.5	35.3	319	8	ADJ98205 Soybean p
40	540.5	35.2	226	8	ADJ25323 Plant ful
41	539	35.1	288	8	ADJ98199 Leek phyt
42	539	35.1	289	8	ADJ94149 Plant ful
43	535.5	34.9	273	8	ADJ24874 Plant ful
44	530.5	34.5	307	8	AAG37869 Arabidops
45	530.5	34.5	307	8	ADJ98168 Thale cre

ALIGNMENTS

RESULT 1
ADJ98164
ID ADJ98164 standard; protein; 304 AA.
XX
AC ADJ98164;
XX
DT 06-MAY-2004 (first entry)
XX
DE Thale cress LTT1 phyto kinase wild-type protein.
XX
KM phyto kinase; tocopherol biosynthesis; plant; drought resistance; LTT1;
KM thale cress; enzyme; wild-type.
XX
OS Arabidopsis thaliana.
XX
PN W02004013312-A2.
XX
PD 12-FEB-2004.
XX
PF 05-AUG-2003; 2003MO-US025276.
XX
PR 05-AUG-2002; 2002US-0400689P.
XX
PR 05-AUG-2003; 2003US-00634548.
XX
PA (MONS) MONSANTO TECHNOLOGY LLC.
XX
PI Norris SR, Lincoln K, Abad MS, Eilers R, Hartsuyker KK;
PI Hirschberg J, Karunananda B, Moshiri F, Stein JC, Valentin HE;
PI Venkatesh TV,
XX
XX WPI; 2004-157125/15.
XX
DR N-PSDB; ADJ98163.
XX
PT New phyto kinase polynucleotides, useful in mediating tocopherol
PT biosynthesis and in producing plants with increased drought resistance.
XX
PS Claim 1, SEQ ID NO 2, 18pp; English.
XX
XX The invention relates to a novel substantially purified nucleic acid
XX molecule encoding a phyto kinase. The nucleic acid molecules and
XX polypeptides of the invention may be useful in mediating tocopherol
XX biosynthesis and in producing plants with increased drought resistance.
XX The current sequence is that of the thale cress LTT1 phyto kinase wild-
XX type protein of the invention.
XX
XX Sequence 304 AA;

Query Match 100.0%; Score 1536; DB 8; Length 304;
 Best Local Similarity 100.0%; Pred. No. 3,9e-162; Indels 0; Gaps 0;
 Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAATPLSPINHQLCRFGNNSLTTHRFCSPEGLISSPCFGLTGMGSAATQLRARRSLISS 60
 DB 1 MAATPLSPINHQLCRFGNNSLTTHRFCSPEGLISSPCFGLTGMGSAATQLRARRSLISS 60
 QY 61 AATNSLHDVGAVAVAGVAVLVSPESLTKNVIOQSRLVHLISGLFVLA MPI 120
 DB 61 AATNSLHDVGAVAVAGVAVLVSPESLTKNVIOQSRLVHLISGLFVLA MPI 120
 QY 121 FSGSTEARYFAFVPLVNGRLVINGLSISPSNMLIKSVTEGRAEELKGPLFVLAALL 180
 DB 121 FSGSTEARYFAFVPLVNGRLVINGLSISPSNMLIKSVTEGRAEELKGPLFVLAALL 180
 QY 181 FSAVFFWRESPIGMIISLAMCGGDIADIMGRKFGSTKIPNPKRSMAGSISMFI FGFPI 240
 DB 181 FSAVFFWRESPIGMIISLAMCGGDIADIMGRKFGSTKIPNPKRSMAGSISMFI FGFPI 240
 QY 241 SIALLYSSSLGYLHMNETTLQRAVMSVAIVVESLPITDQDDNISVPLATILAAYL 300
 DB 241 SIALLYSSSLGYLHMNETTLQRAVMSVAIVVESLPITDQDDNISVPLATILAAYL 300
 QY 301 SFGY 304
 DB 301 SFGY 304

RESULT 2
 ADX91861
 ID ADX91861 standard; protein; 315 AA.

XX AC ADX91861;
 XX DT 21-APR-2005 (first entry)
 XX DB Plant full length insert polypeptide seqid 54545.
 XX KW plant proreccant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX OS Unidentified.
 XX PN US2004034888-A1.
 XX PD 19-FEB-2004.
 XX PF 28-APR-2003; 2003US-00425114.
 XX PR 06-MAY-1999; 99US-00304517.
 XX PR 05-NOV-2001; 2001US-00985678.
 XX PA (LIU/J.) LIU J.
 XX PA (ZHOU/Y.) ZHOU Y.
 XX PA (KOVA/) KOVALIC D K.
 XX PA (SCRE/) SCREEN S E.
 XX PA (TABAKA/) TABAKA J E.
 XX PA (CAO/Y.) CAO Y.
 XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaka JE, Cao Y;
 XX DR WPI; 2004-180333/17.
 XX PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for

PT improving yield.

XX Claim 1; SEQ ID NO 54545; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

XX Sequence 315 AA;

Query Match 100.0%; Score 1536; DB 8; Length 315;
 Best Local Similarity 100.0%; Pred. No. 4.1e-162;
 Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAATPLSPINHQLCRFGNNSLTTHRFCSPEGLISSPCFGLTGMGSAATQLRARRSLISS 60
 DB 12 MAATPLSPINHQLCRFGNNSLTTHRFCSPEGLISSPCFGLTGMGSAATQLRARRSLISS 71
 QY 61 AATNSLHDVGAVAVAGVAVLVSPESLTKNVIOQSRLVHLISGLFVLA MPI 120
 DB 72 AATNSLHDVGAVAVAGVAVLVSPESLTKNVIOQSRLVHLISGLFVLA MPI 131
 QY 121 FSGSTEARYFAFVPLVNGRLVINGLSISPSNMLIKSVTEGRAEELKGPLFVLAALL 180
 DB 132 FSGSTEARYFAFVPLVNGRLVINGLSISPSNMLIKSVTEGRAEELKGPLFVLAALL 191
 QY 181 FSAVFFWRESPIGMIISLAMCGGDIADIMGRKFGSTKIPNPKRSMAGSISMFI FGFPI 240
 DB 192 FSAVFFWRESPIGMIISLAMCGGDIADIMGRKFGSTKIPNPKRSMAGSISMFI FGFPI 251
 QY 241 SIALLYSSSLGYLHMNETTLQRAVMSVAIVVESLPITDQDDNISVPLATILAAYL 300
 DB 252 SIALLYSSSLGYLHMNETTLQRAVMSVAIVVESLPITDQDDNISVPLATILAAYL 311
 QY 301 SFGY 304
 DB 312 SFGY 315

RESULT 3
 ADX91862

ID ADX91862 standard; protein; 301 AA.

XX AC ADX91862;
 XX DT 21-APR-2005 (first entry)
 XX DB Plant full length insert polypeptide seqid 54546.
 XX KW plant proreccant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.

OS Unidentified.
XX US2004034888-A1.
XX 19-FEB-2004.
XX 28-APR-2003; 2003US-00425114.
XX 06-MAY-1999; 99US-00304517.
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/J) LIU J.
XX (ZHOU/Y) ZHOU Y.
XX (KOVALIC D K. KOVALIC D K.
XX (SCREEN S E. SCREEN S E.
XX (TABASKA J E. TABASKA J E.
XX (CAO/Y) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y,
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1; SEQ ID NO 54546; 15bp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.seqdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This is the amino acid sequence of a plant full length insert
XX polypeptide that can be used in the recombinant DNA construct of the
XX invention.
XX
XX Sequence 301 AA;
XX
XX Query Match 99.2%; Score 1523; DB 8; Length 301;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-160;
XX Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 4 TLPLSPINHOICRFENNSLTTHRFCSPPGLISPPCFLTGMSATOLRARRSISSAVA 63
DB 1 TLPLSPINHOICRFENNSLTTHRFCSPPGLISPPCFLTGMSATOLRARRSISSAVA 60
QY 64 TNSLHDVGATVAVALGAYALVLSFESLTGRNVIOQSLSRKLWHLSGLFVLAAMPISFG 123
DB 61 TNSLHDVGATVAVALGAYALVLSFESLTGRNVIOQSLSRKLWHLSGLFVLAAMPISFG 120
QY 124 STEARYFAFVPLVNGRLVINGLSISPNMSLKSVTREGDAEELKPLFYVALALFSA 183
DB 121 STEARYFAFVPLVNGRLVINGLSISPNMSLKSVTREGDAEELKPLFYVALALFSA 180
QY 184 VFPRRESPIGMSIILAMMGCGDIDIMGRKFGSTIPIVNPGRKSNAGSISMFIFGPFISA 243
DB 181 VFPRRESPIGMSIILAMMGCGDIDIMGRKFGSTIPIVNPGRKSNAGSISMFIFGPFISA 240
QY 244 LLYYSSSGYIHHMMWETTLGRVAVMSVATVVESLPIIDQDDNISVPLATILAAVLSFG 303
DB 241 LLYYSSSGYIHHMMWETTLGRVAVMSVATVVESLPIIDQDDNISVPLATILAAVLSFG 300

QY 304 Y 304
DB 301 Y 301
RESULT 4
ID AAG14596 standard; protein; 304 AA.
XX AAG14596;
XX
XX 17-OCT-2000 (first entry)
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 14520.
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XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
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XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
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Query Match 99.7%; Score 1523; DB 3; Length 304;
Best Local Similarity 99.7%; Pred. No. 1.1e-160;
Matches 300; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MDATPLSPINHQCRFGNNSLTTHRFCSPGFLISSPCFGLTGWGSATOLRARRSLISS 60
Cy 61 AVATNSLHDVGATVAVIGGAYALVLSFESLTKRNVIOOSLSRKLVHLSGLPLVLA MPI 120

Db 61 AVATNSLHDVATVAIVGAYALVLSFESLTKRNVQGSRLKVLHLSGLFVLA MPI 120
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Db 121 FSGSTEARVPAFVPLVNGLRVINGLSISPSNMLIKSVTRGRAREELIKGFLFYVALL 180
Qy 181 FSAVFEMRESPIGMSLMMCGGDIADIMGRKFGSTKIPYVPRKSWAGSISMPFEGPFI 240
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Qy 241 SIALLYYSSLGYLHMNWTTLQRVAVMSVATVVSPIPTDLDNDNISVPLATTIAAYL 300
Db 241 SIALLYYSSLGYLHMNWTTLQRVAVMSVATVVSPIPTDLDNDNISVPLATTIAAYL 300
Qy 301 SFGY 304
Db 301 SFGY 304

RESULT 5
AAG14597
ID AAG14597 standard, protein, 260 AA.
AC AAG14597;
XX 17-OCT-2000 (first entry)
DT Arabidopsis thaliana protein fragment SEQ ID NO: 14521.
DE Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS EP1033405-A2.
PN 06-SEP-2000.
PD 25-FEB-2000; 2000EP-00301439.
PF 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
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 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159563P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161992P.

PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 83.5%; Score 1282; DB 3; Length 260;
 Best Local Similarity 98.5%; Pred. No. 6.8e-134;
 Matches 256; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 45 MGSATQRLARRSLISSAVATNSLHDVGATVAVLGGAYVALVLSFESLTGRNVIOQSLSRK 104
 DB 1 MGSATQRLARRSLISSAVATNSLHDVGATVAVLGGAYVALVLSFESLTGRNVIOQSLSRK 60
 QY 105 LVHTLSGLFLVLAAPPIGSGSTEARYFAFPVLVNGGLVINGLSISPSNMLIKSVTEGR 164
 DB 61 LVHTLSGLFLVLAAPPIGSGSTEARYFAFPVLVNGGLVINGLSISPSNMLIKSVTEGR 120
 QY 165 AEBLLKGPLFYVALLSAVFPWRSPGIMISLMMCGDGIADIMGRKFGSTKIPYPR 224
 DB 121 AEBLLKGPLFYVALLSAVFPWRSPGIMISLMMCGDGIADIMGRKFGSTKIPYPR 180
 QY 225 KSNAGSISMPIFGFFISIALLYYSSLGYLHMMNETTLQRYAVVSMVATVSESPIITDQ 284
 DB 181 KSNAGSISMPIFGFFISIALLYYSSLGYLHMMNETTLQRYAVVSMVATVSESPIITDQ 240
 QY 285 DDNISVPLATTLAAVLSFGY 304
 DB 241 DDNISVPLATTLAAVLSFGY 260

RESULT 6
 ADJ98201
 ID ADJ98201 standard; protein; 304 AA.

AC ADJ98201;

DT 06-MAY-2004 (first entry)

DE Rape phytol kinase protein.

XX phytol kinase; tocopherol biosynthesis; plant; drought resistance;

KW enzyme; rape.

OS Brassica napus.

PN WO2004013312-A2.

PD 12-FEB-2004.

XX 05-AUG-2003; 2003WO-US025276.

PF 05-AUG-2002; 2002US-0400689P.

PR 05-AUG-2003; 2003US-00634548.

XX (MONSANTO TECHNOLOGY LLC.

XX Norris SR, Lincoln K, Abad MS, Eilers R, Hartuysen KK;

PI Hirschberg J, Karunanandaa B, Moshiri F, Stein JC, Valentin HE;

PI Venkatesh TV;

XX WPI; 2004-157125/15.

XX New phytol kinase polynucleotides, useful in mediating tocopherol
 PT biosynthesis and in producing plants with increased drought resistance.

XX Claim 1; SEQ ID NO 39; 189pp; English.

XX The invention relates to a novel substantially purified nucleic acid
 CC molecule encoding a phytol kinase. The nucleic acid molecules and
 CC polypeptides of the invention may be useful in mediating tocopherol
 CC biosynthesis and in producing plants with increased drought resistance.
 CC The current sequence is that of a phytol kinase protein of the invention.

XX Sequence 304 AA;

SQ

RESULT 7
ADX91966
ID ADX91966 standard; protein; 319 AA

PT			improving yield.
PS	Claim 1; SEQ ID NO 54630; 15pp; English.		
PX			
CC	The invention describes a recombinant DNA construct comprising a		
CC	polynucleotide consisting of a sequence encoding an amino acid sequence		
CC	available in electronic form from the US patent office at		
CC	ftp.segdata.uspo.gov/sequence.html?docid:200403488. The polynucleotide		
CC	of the invention are also useful in physical arrays of molecules and as		
CC	plant breeding markers. The recombinant DNA construct is useful for		
CC	improving plant tolerance to cold, heat, drought, herbicides, extreme		
CC	osmotic conditions, pathogens or pests, for manipulating growth rate in		
CC	plant cells by modification of the cell cycle pathway, for conferring		
CC	increased resistance to plant disease, for producing galactomannan,		
CC	lignin or plant growth regulators, for increasing the rate of homologous		
CC	recombination in plants, for improving yield by modification of		
CC	photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake		
CC	or by providing improved plant growth and development under at least one		
CC	stress condition or for modifying seed oil or protein yield and/or		
CC	content. This is the amino acid sequence of a plant full length insert		
CC	polypeptide that can be used in the recombinant DNA construct of the		
CC	invention.		
SQ	Sequence 319 AA:		
XX			
XX			
Query Match	82.4%; Score 1266; DB 8; Length 319;		
Best Local Similarity	81.4%; Pred. No. 5.5e-132;		
Matches 250; Conservative	24; Mismatches 27; Indels 6; Gaps 2;		
QY	1 MAATLPSPINHOLCRGN--SLTTRFCSPGLISSPCFGLTGMSATOLRARSL 57		
DB	16 MAALPLSPVSHOUCRSNRFNTAMTPRCSP--VSFCYIGVKIGSSQLRAHPL 72		
QY	58 ISSAATNSLDHDGATAVALGAAYALVFSFSTIKRNVIQGSLSRLVHLISGLFLVA 117		
DB	73 ISSASTDYLLHDGATAVALVSGAVLVLFESITKRDVLPQRLSRLVHLISGLPALS 132		
QY	118 WPIFGSGTEARYPAAPVLVNGLRVLVNGISISPNMLKSVTREGABELKGPLEYYL 177		
DB	133 WPIFSASTERYPAAFPVLVNGLRVLVNGLSVSPNSTLIOSVIREGRBELKGPLEYVL 192		
QY	178 ALLESAVFEPRESPIGWISLAMCGGGDIADINDIGRKSGTKIPNPCKSMAGSIWTFIG 237		
DB	193 ALLVAARVPFRDSTGTGISLAMCGGGIADINGRKTSYKIPNPKKSLAGSISWEIFG 252		
QY	238 FFISIALLYTYSSISGLYLMNMETTLORVANWSVATVESLPIQTDDDNISVPLATILA 297		
DB	253 FFIISIGILYYSSISGLYLMNMETTFRRVALVSVATIVESLPITDQIDDVSVPLATILA 312		
QY	298 AYLSPGY 304		
DB	313 AYLSFGY 319		
RESULT 8			
ID	ADJ98166 standard; protein; 226 AA.		
AC	ADJ98166;		
DT	06-MAY-2004 (first entry)		
DE	Thale cress LTT1 phytoI kinase mutant protein.		
KX	phytoI kinase; tocopherol biosynthesis; plant; drought resistance; LTT1;		
XK	thale cress; enzyme; mutant; mutain.		
OS	Arabidopsis thaliana.		
Key	Location/Qualifiers		
Misc-difference 226	/note= "Wild-type Ser, Trp is substituted for Ser, SHOP"		

PN WO2004013312-A2.
 XX
 PD 12-FEB-2004.
 XX
 XX 05-AUG-2003; 2003WO-US025276.
 PF
 XX 05-AUG-2002; 2002US-0400689P.
 PR
 XX 05-AUG-2003; 2003US-00634548.
 XX
 PA (MONSANTO TECHNOLOGY LLC.
 PI Norris SR, Lincoln K, Abad MS, Eljers R, Harteuyker KK,
 PI Hirschberg J, Karunanandaa B, Moshiri F, Stein JC, Valentin HR,
 PI Venkatesh TV;
 XX
 DR WPI; 2004-157125/15.
 DR N-PSDB; ADJ98165.
 PT
 PT New phyto kinase polynucleotides, useful in mediating tocopherol
 biosynthesis and in producing plants with increased drought resistance.
 XX
 PS Example 2; SEQ ID NO 4; 189pp; English.
 CC The invention relates to a novel substantially purified nucleic acid
 CC molecule encoding a phyto kinase. The nucleic acid molecules and
 CC polypeptides of the invention may be useful in mediating tocopherol
 CC biosynthesis and in producing plants with increased drought resistance.
 CC The current sequence is that of the thale cress LTT1 phyto kinase mutant
 CC protein of the invention.
 XX
 SQ Sequence 226 AA;
 Query Match 74.2%; Score 1140; DB 8; Length 226;
 Best Local Similarity 100.0%; Pred. No. 3.8e-118;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAATPLSPINHQLCRFGNNSLTTRFCSPGLISSPCFGLTGMGSAATOLRARRSLISS 60
 DB 1 MAATPLSPINHQLCRFGNNSLTTRFCSPGLISSPCFGLTGMGSAATOLRARRSLISS 60
 QY 61 AVATNSLHDVAGATVAVVGAYALVLSFESLTKRVNIOOSLSRKVHLISGLLPYLA 120
 DB 61 AVATNSLHDVAGATVAVVGAYALVLSFESLTKRVNIOOSLSRKVHLISGLLPYLA 120
 QY 121 FSGSTEARYPFAFVPLVNGRLVINGLSISPSNMLIKSVTRREGRAEELIKGFLPYVAL 180
 DB 121 FSGSTEARYPFAFVPLVNGRLVINGLSISPSNMLIKSVTRREGRAEELIKGFLPYVAL 180
 QY 181 FSAVFPWRESPIGMI SLAMCGGDIADIMGRKFGSTKIPYVPRKS 226
 DB 181 FSAVFPWRESPIGMI SLAMCGGDIADIMGRKFGSTKIPYVPRKS 226
 RESULT 9
 ID ADX91971 standard; protein; 306 AA.
 XX
 AC ADX91971;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polypeptide seqid 54635.
 XX
 KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 XX
 OS Unidentified.

XX US2004034888-A1.
 PN
 XX
 PD 19-FEB-2004.
 XX
 XX 28-APR-2003; 2003US-00425114.
 PF
 XX 06-MAY-1999; 99US-00304517.
 PR
 XX 05-NOV-2001; 2001US-00985678.
 XX
 PA (LTUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABAS/) TABASKA J E.
 PA (CAO/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 PI
 DR WPI; 2004-180133/17.
 DR
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 54635; 15pp; English.
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docID:200403488. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 XX
 SQ Sequence 306 AA;
 Query Match 56.6%; Score 870; DB 8; Length 306;
 Best Local Similarity 56.7%; Pred. No. 7.8e-88;
 Matches 174; Conservative 51; Mismatches 72; Indels 10; Gaps 2;
 QY 2 AATPLSPINHQLCRFGNNSLTTRFCSPGLISSPCFGLTGMGSAATOLRARRSL 57
 DB 6 AATMSLS-----LSFTPIISRHYSAVFPPEPRFLFSPILPTTSRPPILYRADORATA 59
 QY 58 ISSAVATNSLHDVAGATVAVVGAYALVLSFESLTKRVNIOOSLSRKVHLISGLLPYLA 117
 DB 60 LSATRVATNSIFRDRRAASVAVGAYALVFTFDILTKELIQNLSRKVHLISGLLPYLA 119
 QY 118 WPIFSGSTEARYPFAFVPLVNGRLVINGLSISPSNMLIKSVTRREGRAEELIKGFLPYVAL 177
 DB 120 WPIFSGSTEARYPFAFVPLVNGRLVINGLSISPSNMLIKSVTRREGRAEELIKGFLPYVAL 179
 QY 178 ALTSVAVFPWRESPIGMI SLAMCGGDIADIMGRKFGSTKIPYVPRKSWMGSI 237
 DB 180 MLCALVFPWRESPIGMI SLAMCGGDIADIMGRKFGSTKIPYVPRKSWMGSI 239
 QY 238 FFISATLTYYSLSGLYHMMWETTLQRYAVMSVAVTESPITDQDNISVPLATIIA 297
 DB 240 FTISGMLTYYSALGQIDLDGTYLHRVAFISVAVTESPISMLIDDNISVPLASMLA 299

Qy 298 AYLSFGY 304
 |||:
 Db 300 AYLTFGH 306

RESULT 10

ID ADJ98203 standard; protein; 298 AA.
 XX ADJ98203;
 AC ADJ98203;
 DT 06-MAY-2004 (first entry)
 XX
 DE Upland cotton phyto kinase protein.
 XX
 KM phyto kinase; tocopherol biosynthesis; plant; drought resistance;
 KM enzyme; upland cotton.
 XX
 OS Gossypium hirsutum.
 XX
 PN MO2004013312-A2.
 XX
 PD 12-FEB-2004.
 XX
 PF 05-AUG-2003; 2003WO-US025276.
 XX
 PR 05-AUG-2002; 2002US-0400689P.
 PR 05-AUG-2003; 2003US-00634548.
 XX
 PA (MONS) MONSANTO TECHNOLOGY LLC.
 XX
 PI Norris SR, Lincoln K, Abad MS, Ellers R, Hartuysker KK;
 PI Hirschberg J, Karunanandaa B, Moshiri F, Stein JC, Valentin HE;
 PI Venkatesh TV;
 XX
 DR WPI; 2004-157125/15.
 XX
 DR

PT New phyto kinase polynucleotides, useful in mediating tocopherol
 PT biosynthesis and in producing plants with increased drought resistance.
 XX
 PS Claim 1; SEQ ID NO 41; 189pp; English.

CC The invention relates to a novel substantially purified nucleic acid
 CC molecule encoding a phyto kinase. The nucleic acid molecules and
 CC polypeptides of the invention may be useful in mediating tocopherol
 CC biosynthesis and in producing plants with increased drought resistance.
 CC The current sequence is that of a phyto kinase protein of the invention.
 CC
 XX

Sequence 298 AA;

Query Match 56.2%; Score 864; DB 8; Length 298;
 Best Local Similarity 60.1%; Pred. No. 3.5e-87;

Matches 167; Conservative 46; Mismatches 65; Indels 0; Gaps 0;

Qy 27 FCSFGFLISSPCFGLTGMGSAATOLRARRSLISSAVATNSLHDVGAATVAVGAYATL 86
 |||:
 Db 21 PPPPFLSLPILPTTSRFPILYRAQRAIALSAVAVTASITRDPAAASVPAAGAYALVF 80
 |||:
 Qy 87 SFESLTKRNVIOQSLSKLVHLSGLFLVAMPFSGSTEARYFAFVPLVNGRLTVNG 146
 |||:
 Db 81 TFDILTOGRELIOQNSRLKLVHLSGLFLVAMPFSGSTEARYFAFVPLVNGRLTVNG 140
 |||:
 Qy 147 LSISNSMLIKSVTRREGRABELKGPLFYVALALFSAPFMRRESITGMSLMMCGGDCI 206
 |||:
 Db 141 LSLTDDOELIKSVTRREGRABELKGPLFYVALALFSAPFMRRESITGMSLMMCGGDCI 200
 |||:
 Qy 207 ADIMRKKGSTKIPYNPKSNAGSISMFIPGFISIALLYSSLSGYLHAMWETTLQRYA 266
 |||:
 Db 201 ADIIRKKGSSKIPYNOSKSNAGSISMFVSGFTISIGMLYYISALGYLQDMGTLHRYA 260
 |||:
 Qy 267 MVSNAVATVESLPTDQDDNISVPLATILAAVLSFGY 304
 |||:
 Db 261 FLSLVATVESLPTISMLIDNISVPLASMLAAVLTFGH 298

RESULT 11

ID ADJ98207 standard; protein; 302 AA.

XX ADJ98207;
 AC ADJ98207;
 DT 06-MAY-2004 (first entry)
 XX
 DE Soybean phyto kinase protein.
 XX
 KM phyto kinase; tocopherol biosynthesis; plant; drought resistance;
 KM enzyme; soybean.
 XX
 OS Glycine max.
 XX
 PN MO2004013312-A2.
 XX
 PD 12-FEB-2004.
 XX
 PF 05-AUG-2003; 2003WO-US025276.
 XX
 PR 05-AUG-2002; 2002US-0400689P.
 PR 05-AUG-2003; 2003US-00634548.
 XX
 PA (MONS) MONSANTO TECHNOLOGY LLC.
 XX
 PI Norris SR, Lincoln K, Abad MS, Ellers R, Hartuysker KK;
 PI Hirschberg J, Karunanandaa B, Moshiri F, Stein JC, Valentin HE;
 PI Venkatesh TV;
 XX
 DR WPI; 2004-157125/15.
 XX
 DR

PT New phyto kinase polynucleotides, useful in mediating tocopherol
 PT biosynthesis and in producing plants with increased drought resistance.
 XX
 PS Claim 1; SEQ ID NO 45; 189pp; English.

CC The invention relates to a novel substantially purified nucleic acid
 CC molecule encoding a phyto kinase. The nucleic acid molecules and
 CC polypeptides of the invention may be useful in mediating tocopherol
 CC biosynthesis and in producing plants with increased drought resistance.
 CC The current sequence is that of a phyto kinase protein of the invention.
 CC
 XX

Sequence 302 AA;

Query Match 55.8%; Score 857.5; DB 8; Length 302;
 Best Local Similarity 60.6%; Pred. No. 1.9e-86;

Matches 175; Conservative 44; Mismatches 51; Indels 19; Gaps 5;

Qy 19 NNSLTTT--RF-CSPGFLISSPCFGLTGMGSAATOL--RARRSLISSAVATNSLHDVGA 73
 |||:
 Db 26 NSPTTNTVRLCSP-----GVPPAVRLDRLPRFVPGAGA-EDLLYNAGA 71
 |||:
 Qy 74 TVAVLGGAYALVLSFESLTKRNVIOQSLSKLVHLSGLFLVAMPFSGSTEARYFAF 133
 |||:
 Db 72 TVGVLGGAYALVRAFDLITRNNILQOGLSRKLVHLSGLFLVAMPFSGSTEARYFAF 131
 |||:
 Qy 134 VPLVNGRLTVNGSLISPSNMLIKSVTRREGRABELKGPLFYVALALFSAPFMRRESPIG 193
 |||:
 Db 132 VPLVNGRLTVNGSLISPSNMLIKSVTRREGRABELKGPLFYVALALFSAPFMRRESPIG 191
 |||:
 Qy 194 MISLMMCGGDCIADIMRKKGSTKIPYNPKSNAGSISMFIPGFISIALLYSSLSGY 253
 |||:
 Db 192 VISLMMCGGDCIADITGRYSGMKIPYNEHKSLSAGSMMLVFGFLVISIGMLYYISVYGH 251
 |||:
 Qy 254 LHAMWETTLQRYAVNAVSVATVESLPTDQDDNISVPLATILAAVLSF 302
 |||:
 Db 252 VQDMASTLPRVAFISFVATLVESLPTTKVDDNISVPLATMAVAAPFTF 300

RESULT 12

```

ADJ98208
ID ADJ98208 standard; protein; 314 AA.
XX
AC ADJ98208;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rice phytoI kinase protein.
XX
KW phytoI kinase; tocopherol biosynthesis; plant; drought resistance;
KM enzyme; rice.
XX
OS Oryza sativa.
XX
PN MO2004013312-A2.
XX
PD 12-FEB-2004.
XX
PF 05-AUG-2003; 2003WO-US025276.
XX
PR 05-AUG-2002; 2002US-0400689P.
PR 05-AUG-2003; 2003US-00634548.
XX
PA (MONS ) MONSANTO TECHNOLOGY LLC.
XX
PI Norris SR, Iancola K, Abad MS, Eilers R, Hartuyker KK;
PI Hirschberg J, Karunanandaa B, Moshiri F, Stein JC, Valentin HE;
PI Venkatesh IV;
DR MPI; 2004-157125/15.
XX
PT New phytoI kinase polynucleotides, useful in mediating tocopherol
XX biosynthesis and in producing plants with increased drought resistance.
XX
PS Claim 1; SEQ ID NO 46; 189pp; English.
XX
CC The invention relates to a novel substantially purified nucleic acid
XX molecule encoding a phytoI kinase. The nucleic acid molecules and
XX polypeptides of the invention may be useful in mediating tocopherol
XX biosynthesis and in producing plants with increased drought resistance.
XX CC The current sequence is that of a phytoI kinase protein of the invention.
XX
SQ Sequence 314 AA;
Query Match 51.5%; Score 791.5; DB 8; Length 314;
Best Local Similarity 51.1%; Pred. NO. 4,7e-79; Indels 11; Gaps 4;
Matches 159; Conservative 60; Mismatches 81;
2 AATLPLSPINQLCR---FGNNSL-----TTRFCSPGLISSPCFGLT-GMGSAATQURA 53
3 AARVVDVVRHPPCGSSVVAASSLSLSKSLASPAAAAASMRRLVGVGA---A 59
4 RRLISSAVAINSLHDGATVAVTGAYALVLSRESLTNRVITOOSLSRKLVLHLSGL 113
5 PAVVAALASATPAARDCAAATLLITAGAVSLVARPDGLTARLLIOMNSRKIVHLSGLV 119
6 PAVVAALASATPAARDCAAATLLITAGAVSLVARPDGLTARLLIOMNSRKIVHLSGLV 119
114 PVLAMPISGSGTEARYPAFVPLVNGLRVINGLSISPSMUKSVTEGREGAEEILKGPL 173
120 FVSSPPLFNSNSTEARFAAIVPLNLCIRLLTGLISTDGLAVKSVTEGKEEELRGPL 179
174 FVVLALFSAVPEFMRBSPIGMISLAMCGDGIADIMGRKFGSKTIPYPRKSMAGSISM 233
180 YVIVVLAVSVLFWFGSPGIVISLMSGSGDFADIVGRYSATKLPRFNKSWIGSISM 239
234 FTFGFFISIALIYYSSIGYLMNMETTLQRYVAMSVAVTVESLPITDQLDNNTISVPLA 293
240 FISGFLSLALMLFYFSCIGYFTVCWDLALGKLALVALAATVVEICPVNDVDSIVPLA 299
QY 294 TILAAVLSFGY 304
DB 300 TMLAAVLSFGY 310

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RESULT 13
ADX93121
ID ADX93121 standard; protein; 332 AA.
XX
AC ADX93121;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polypeptide seqid 55785.
XX
KW plant protectant; plant growth regulator; gene therapy; plant;
KM recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KM galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
KM protein content.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIU/J) LIU J.
PA (ZHOU/J) ZHOU Y.
PA (KOVA/J) KOVALIC D K.
PA (SCRE/J) SCREEN S E.
PA (TABASKA/J) TABASKA J E.
PA (CAO/Y) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SR, Tabaska JE, Cao Y,
DR MPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
XX pest, cold, drought, herbicides, extreme osmotic conditions, pathogens or
XX for conferring increased resistance to plant disease, or for
XX improving yield.
XX
PS Claim 1; SEQ ID NO 55785; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp://seeddata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This is the amino acid sequence of a plant full length insert
XX polypeptide that can be used in the recombinant DNA construct of the
XX invention.
XX
SQ Sequence 332 AA;
Query Match 51.5%; Score 791.5; DB 8; Length 332;
Best Local Similarity 51.1%; Pred. NO. 5e-79; Indels 11; Gaps 4;
Matches 159; Conservative 60; Mismatches 81;

```


Query Match	51.5%	Score 791.5	DB 8	Length 657
Best Local Similarity	51.1%	Pred. No. 1.4e-78		
Matches 159	Conservative 60	Mismatches 81	Indels 11	Gaps 4

Query Match	51.5%	Score 791.5;	DB 8;	Length 803;
Best Local Similarity	51.1%;	Pred. No. 1.8e-78;		

Matches 159; Conservative 60; Mismatches 81; Indels 11; Gaps 4;

```

QY      2  AATLEPLSPNHOLCR---FGNNSL-----TTHPFCSGFPLISSPCFICLT-GMSAQQLRA 53
Db      492  AARREVDVVRHPPCCSSVVAASSLLSRKSLRAASAAAAASMRRLVVGVAAL---A 548
QY      54  RRSLISSAVAINSLHDVGATVAVLCGAYALVLSFESLTKRNVYQOQSLSKLVHIIISGL 113
Db      549  PAVAAALASATPAALRDCATLTLLTGAAGSLVRAAFGLTARRRIEONLSRKIVHVISGYL 608
QY      114  FVLAMPFIFGSGTEARFAAFVFLVNLGRLATVINGLSISPSMILIKSVYTRGGRABEELKGPL 173
Db      609  FMSSMRPLPENSSTEARFAALVPLLNCRILRLTYTGLRSTDEALVKSVYTRGGRKPELLRGPL 668
QY      174  FYVYLLALBSAVFFMRBSPITGMITSLAMCGGDIADIMGRKFGSTKLPYPRKSMASISIM 223
Db      669  YVYIVLVSLVALFWRQSPIGIVISLMSMGDGDADIVGRYGSACKLPFNENKSMWISISIM 728
QY      234  FIFGFFISIALLYVYSGSLGVLHMMNMTTQLQRVAVMSVAVTVASLEPIITQOLDNISVPLA 293
Db      729  FLSGFLLSALMLFYFSCGLGYFTYCCMDLALGKLALVALAATVVECPVNDVDDNISVPLA 788
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Search completed: March 16, 2006, 19:49:02
Job time : 92 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 16, 2006, 15:34:32 ; Search time 7827 Seconds
(without alignments)
7923.369 Million cell updates/sec

Title: US-10-634-548-1

Perfect score: 1091
Sequence: 1 aaaaaagaataaatacaca.....ccgaactacaatgttcc 1091

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmb1:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_cm:*
5: gb_ov:*
6: gb_dac:*
7: gb_ph:*
8: gb_pr:*
9: gb_to:*
10: gb_sts:*
11: gb_gy:*
12: gb_un:*
13: gb_vl:*
14: gb_hlg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1075	98.5	1091	15	AY085036 Arabidops
2	1051.4	96.4	1072	15	BT004006 Arabidops
3	1002	91.8	1004	15	BT021123 Arabidops
4	404	37.0	93045	15	AT132M21 Arabidops
5	161.4	14.8	1002	15	AK061265 Arabidops
6	147	13.5	1218	15	AK10748 Arabidops
7	144.8	13.3	1059	15	AK109049 Arabidops
8	138	12.6	1211	15	AK176090 Arabidops
9	136.4	12.5	1360	15	AK176217 Arabidops
10	134.8	12.4	1162	15	AY087555 Arabidops
11	127	11.6	436	15	AK063069 Arabidops
12	86	7.9	110000	14	CR954207 Oryza sat
13	79	7.2	110000	14	CR954207 Oryza sat
14	67.2	6.2	81672	15	AB020755 Arabidops
15	67	6.1	7218	6	166494 Sequence 14
16	65.8	6.0	3143	15	AK065924 Arabidops
17	65.8	6.0	95419	14	OSIG00051 Arabidops
18	65.8	6.0	110000	15	AP008210_342 Arabidops

19	65.8	6.0	190432	15	OSJN00032 Arabidops
20	58.8	5.4	477	10	BV151380 Arabidops
21	58.8	5.4	465	10	BV151381 Arabidops
22	58.8	5.4	493	10	BV151387 Arabidops
23	58.8	5.4	506	10	BV151376 Arabidops
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27	58.8	5.4	515	10	BV151385 Arabidops
28	58.8	5.4	516	10	BV151377 Arabidops
29	58.8	5.4	518	10	BV151363 Arabidops
30	58.8	5.4	529	10	BV151386 Arabidops
31	57.2	5.2	513	10	BV151378 Arabidops
32	46.8	4.3	14603	2	AC116989 Arabidops
33	46.8	4.2	200983	9	AC116989 Arabidops
34	45.8	4.2	129719	8	AC158113 Arabidops
35	45.4	4.2	81410	8	AC073594 Arabidops
36	45.2	4.1	93331	8	AC107392 Arabidops
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ALIGNMENTS

RESULT 1	AY085036	1091 bp	mrna	linear	PLN 14-APR-2003
LOCUS	AY085036	Arabidopsis thaliana clone 125255	mrna	complete sequence.	
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ACCESSION	AY085036	GI:21403746			
VERSION	AY085036.1				
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SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	Haas, B.J., Volkov, N., Town, C.D., Troughan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O., and Salzberg, S.L.				
AUTHORS	Full-length messenger RNA sequences greatly improve genome annotation				
TITLE	Genome Biol. 3 (6), RESEARCH0029 (2002)				
JOURNAL	12093376				
PUBMED	2 (bases 1 to 1091)				
REFERENCE	Brover, V., Troughan, M., Alexandrov, N., Lu, Y.-P., Flavell, R., and Feldmann, K.				
AUTHORS	Full-length cDNA from Arabidopsis thaliana				
TITLE	Unpublished				
JOURNAL	3 (bases 1 to 1091)				
REFERENCE	Brover, V., Troughan, M., Alexandrov, N., Lu, Y.-P., Flavell, R., and Feldmann, K.				
AUTHORS	Direct Submission				
TITLE	Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA				
COMMENT	This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and GenBank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA				

(Signal), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

FEATURES

Source

Location/Qualifiers

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SLPTDLDNISVPLATILAAVLSFG"

CDS

Query Match 91.8%; Score 1002; DB 15; Length 1004;
Best Local Similarity 100.0%; Pred. No. 2.5e-266;
Matches 1002; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

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RESULT 4

ATT32M21

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

TITLE

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DEFINITION	Oryza sativa (japonica cultivar-group) cDNA clone:002-170-G04, full-length insert sequence.			
ACCESSION	AKI10748			
VERSION	AKI10748.1			
KEYWORDS	FLI CDNA; oligo capping.			
SOURCE	Oryza sativa (japonica cultivar-group)			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzae; Oryza.			
REFERENCE	1			
AUTHORS	The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-Length cDNA Project Team.; Kikuchi,S., Satoh,K., Nagata,T., Kawagashita,N., Doi,K., Kimimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Koike,K., Nemiki,T., Ohneda,E., Yahagi,M., Suzuki,K., Ii,C., Oheuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group.; Okono,Y., Murakami,K., Ikeda,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsumoda,Y., Kurotaki,T., Kodama,T., Maeda,H., Kobayashi,M., Xie,Q., Lu,M.,			

TITLE	JOURNAL	COMMENT
<p>Naikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikawa, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Mura, J., Kusunegi, T., Oka, M., Ryu, R., Ueda, M., Matubara, K., RIKEN: Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hasehime, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Kondo, S., Kono, H., Miyazaki, A., Otsu, N., Ota, Y., Sato, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.</p> <p>Collection, mapping, and annotation of over 28,000 cDNA clones from <i>Japonica</i> rice</p> <p>Science 301 (5631), 376-379 (2003)</p> <p>12869764</p> <p>2 (bases 1 to 1218)</p> <p>Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hasehime, W., Hayashizaki, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kigawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusunegi, T., Li, C., Lu, M., Mizuno, H., Matubara, K., Matsumura, T., Mura, J., Miyazaki, A., Mura, K., Murakami, K., Murakami, M., Nagata, T., Nakamura, M., Namiki, T., Naikawa, R., Nishikawa, R., Nishikawa, R., Nomura, K., Numaaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Otsu, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Sato, R., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.</p> <p>Direct Submissions</p> <p>Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: kiki@nias.affrc.go.jp).</p> <p>Tel: 81-29-838-7007, Fax: 81-29-838-7007</p> <p>This clone is one of the 28K full-length cDNA clones from <i>Japonica</i> rice.</p> <p>url: http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_cDNA_Project_Team:kikuchi.S.,sato.h.,nagata.T.,kawagashira.N.,doi.K.,kishimoto.N.,yazaki.J.,ishikawa.M.,yamada.H.,oka.H.,hotta.I.,kojima.K.,namiki.T.,ohneda.E.,yahagi.W.,suzuki.K.,li.C.,ohsaki.K.,shishiki.T.,and.yamamoto.M.</p> <p>PAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusunegi, T., Lu, M., Masuda, H., Mura, J., Mizuno, K., Naikawa, R., Nishikawa, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matubara, K., and Murakami, K.</p> <p>Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hasehime, W., Hayashizaki, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsumura, T., Miyazaki, A., Mura, M., Nakamura, M., Nishikawa, K., Nomura, K., Numaaki, R., Ohno, M., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.</p> <p>location/Qualifiers</p> <p>1. 1218</p> <p>/organism="Oryza sativa (japonica cultivar-group)"</p> <p>/mol_type="mRNA"</p> <p>/cultivar="Nipponbare"</p>		

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Matches 380; Conservative 0; Mismatches 345; Indels 6; Gaps 2

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Db	555	TTCGCTACGTATATTTCTGAGAGACATCTCCCATTTCAATGCGAGTATTTGGACATTTGT	614
Oy	709	GTGTGGCGATGSAATAGCTGATATPAATGGGACGTAAATTGGGCTCACTAAGATACCTT	768
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Oy	769	ACAAACCCAGAAAGATTTGGGCGAGAGACATCTCATGTTCATCTTTCGAGCTTCTTCACT	828
Db	675	ACAACCCGATPAAGCTTATGCTGGATCCATTTGCAATGTCTTAACTGCTGTTTCTTGCAT	734
Oy	829	CCATGTGACTTACTTATCTTATCTCAACGCTTGGGTACTTCAACATGAACTGGGAAACGA	888
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Oy	889	CTTTCAGAGATGACATAGTGTCAATAGTGTGCGACAGGTAGTCAGTGTGCTAACCATCA	948
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Oy	1009	GTTTCGATAT 1019	
Db	912	TTTTCTATTAT 922	

REFERENCE AUTHORS

Ehrhartoideae; Oryzeae; *Oryza*.

1. The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kijima, K., Namiki, T., Ohneda, Y., Yabagi, M., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Oono, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tanoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niihara, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Mura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN: Kawai, J., Carrinoni, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, S., Hayashi, N., Imotani, K., Inai, Y., Ichihashi, K., Kaga, I., Kondo, S., Komori, H., Miyazaki, A., Otsu, N., Oca, Y., Kaga, I., Sato, K., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.

JOURNAL
PUBMED
Science 301 (5631), 376-379 (2003)
12863764
2 (Pages 1 to 1059)
REFERENCE

TITLE Direct Submission
JOURNAL Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp).

COMMENT This clone is one of the 28K full-length cDNA clones from *Japonica*

URL : http://cdna01.dna.affrc.go.jp/cDNA/NIRS_Rice_Full-length_cDNA_Project_Team:Rkuchi,S.,Satoh,K.,Negata,T.,Kawagashira,N.,Doi,K.,Kishimoto,N.,Yazaki,J.,Ishikawa,M.,Yamada,H.,Ooka,H.,Hotta,I.,Kojima,K.,Nemiki,T.,Ohneda,E.,Yahagi,W.,Suzuki,K.,Li,C.,Ohtsuki,K.,Shienkai,T. and Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, K., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusnegi, T., Lu, M., Masuda, H., Miura, J., Mituno, K., Nakikawa, R., Nikiwa, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Teunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Haseizume, W., Hayashida, K., Hayatsu, N., Hizumoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imochi, K., Ishii, Y., Itoh, N., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirizono, T., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Mureta, M.,

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RESULT 9
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK176217 1360 bp mRNA linear PLAN 09-SEP-2004
Arabidopsis thaliana mRNA, complete cds, clone: RAFL23-09-006.
AK176217.1 GI:51970575
FLI CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

1
Totoaki, Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A.,
Narusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, N., Oishi, K.,
Kohara, Y., Kobayashi, M., Toyoda, A., Sakaki, Y., Sakurai, T., Iida, K.,
Akiyama, K., Satou, M., Toyoda, T., Konagaya, A., Carninci, P.,
Kawai, J., Hayashizaki, Y., and Shinozaki, K.
Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs
unpublished
2 (bases 1 to 1360)
Totoaki, Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A.,
Narusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, N., Oishi, K.,
Kohara, Y., Kobayashi, M., Toyoda, A., Sakaki, Y., Sakurai, T., Iida, K.,
Akiyama, K., Satou, M., Toyoda, T., Konagaya, A., Carninci, P.,
Kawai, J., Hayashizaki, Y., and Shinozaki, K.

Kawai, J., Hayashizaki, Y. and Shinozaki, K.
Direct Submission
Submitted (06-SEP-2004) Motoaki Seki, RIKEN Genomic Sciences
Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa
230-0045, Japan (E-mail:msk@gscc.riken.jp, Tel:81-45-503-9655,
URL: http://range.gsc.riken.jp/, Fax:81-45-503-9586)
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al. (1998) Plant J. 15:707-720;
Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI
and XhoI was ligated to modified lambda phage vector (Carninci et
al. (2001) Genomics 77:79-90) digested with BamHI and SalI. This
clone is in a modified phage vector.
Please visit our web site (http://range.gsc.riken.jp/) for further
details.

FEATURES
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ORIGIN
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Db      1039 TCTAATATA 1048

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VERSION   AY087555.1 GI:21406293
KEYWORDS  FLI CDNA.
SOURCE    Arabidopsis thaliana (chale crees)
ORGANISM  Arabidopsis thaliana

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REFERENCE
AUTHORS Haas,B.J., Volkovskiy,N., Town,C.D., Troughan,M., Alexandrov,N.,
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
Genome Biol. 3 (6), RESEARCH0029 (2002)
12093376

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TITLE
JOURNAL PubMed
REFERENCE 2 (bases 1 to 1162)
AUTHORS Brover,V., Troughan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Full-length cDNA from Arabidopsis thaliana
Unpublished
3 (bases 1 to 1162)

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TITLE
JOURNAL Direct Submission
REFERENCE Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
AUTHORS Malibu, CA 90265, USA
COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to Tigr and Genbank. The following quality assessment of
this set was done by comparison with known proteins: two percent of
the clones are estimated to be 5'-truncated; less than one percent
are 3'-truncated; approximately two percent represent alternative
splice variants, including unspliced introns and spliced exons; one
percent may contain premature stop codons; five percent may have
frame shifts in a coding region. A sequence is considered to be
5'-truncated if it lacks the translation initiation start (ATG). A
sequence is considered to be 3'-truncated if it lacks the
C-terminal end of the encoded protein. Please note that these cDNA
sequences are derived from the Ws or later ecotypes and therefore
may contain polymorphisms when compared to sequences from Col-0.
Genet carried out the library production and sequencing of the
full-length clones. Ceres, Inc. carried out the clustering of the
5' sequences, selection of clones, and sequence assembly.
Location/Qualifiers
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FEATURES
Source

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ORIGIN

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Query Match 12.4%; Score 134.8; DB 15; Length 1162;
Best Local Similarity 50.0%; Pred. No. 7e-26;
Matches 365; Conservative 0; Mismatches 362; Indels 3; Gaps 1;

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RESULT 11
AK063069
LOCUS
DEFINITION
AK063069 436 bp mRNA linear PLN 24-JUL-2003
Oryza sativa (japonica cultivar-group) cDNA clone:001-110-G11, full
insert sequence.

ACCESSION
AK063069
VERSION
AK063069.1 GI:32973087
KEYWORDS
FLI CDNA; oligo-capping.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
1
The Rice Full-length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team;
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group, Ohtsuki, K., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kuroseki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J.,
Iweda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN;
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hasehida, K., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Oosato, N., Oka, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M., and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
2 (bases 1 to 436)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hasehida, K.,
Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T.,
Hori, F., Hotta, I., Iida, J., Iida, Y., Iweda, R., Imamura, K.,
Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
Kawagashira, N., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kurihara, C., Kuroseki, T., Kusumegi, T., Li, C., Lu, M.,
Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,
Namiki, T., Narikawa, R., Nishikura, J., Nishi, K., Nomura, K.,
Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,
Oosato, N., Oka, Y., Ohtsuki, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K.,
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,
Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
Yamada, H., Yamamoto, M., Yasunishi, A., Yasaki, J., Yokomizo, S., and
Yoshimura, A.
Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
rice.
URL: <http://cdna01.dna.affrc.go.jp/cdna/>
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and
Yamamoto, M.
FAIS Genome Sequencing & Analysis Group: Ohtsuki, Y., Iida, Y.,
Fujimura, T., Iweda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,

Kodama, T., Kuroseki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
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Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K., and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hasehida, K., Hayashizaki, K., Hayatsu, N., Hiramoto, K.,
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Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Oosato, N.,
Oka, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
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Yasunishi, A., and Hayashizaki, Y.
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FEATURES
source
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DEFINITION
Ostreococcus tauri strain OTH0595, *** SEQUENCING IN PROGRESS ***.
ACCESSION
CR954207 GI:70062434

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LOCUS
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DEFINITION
Ostreococcus tauri strain OTH0595, *** SEQUENCING IN PROGRESS ***.
ACCESSION
CR954207 GI:70062434

KEYWORDS	HTGS, PHASE2, green alga, whole genome shotgun.
SOURCE	Ostreococcus tauri
ORGANISM	Eukaryota, Viridiplantae; Chlorophyta; Prasinophyceae; Mamiellales; Mamiellaceae; Ostreococcus.
REFERENCE	1 (bases 1 to 739027)
AUTHORS	Derelle, E., Ferraz, C., Rombauts, S., Rouze, P., Worden, A.Z., Patensky, F., Desroche, S., Echeynle, S., Cooke, R., Robbens, S., Wyts, J., Saey, Y., Jabbari, K., Bowler, C., Ball, S., Ral, J.P., Bouger, F.Y., Piganeau, G., De Baets, B., Picard, A., Delseny, M., Demalle, J., Van de Peer, Y. and Moreau, H.
TITLE	Genome analysis of the smallest free-living eukaryote <i>Ostreococcus tauri</i> unveils unique genome heterogeneity
JOURNAL	Nature (2005) In press
REFERENCE	2 (bases 1 to 739027)
AUTHORS	Rombauts, S., Derelle, E., Ferraz, C., Van de Peer, Y. and Moreau, H.
TITLE	Direct Submission
JOURNAL	Submitted (30-APR-2005)
COMMENT	On Jul 7, 2005 this sequence version replaced gi:62990099.

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RESULT 14
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 DEFINITION AB020755 BA000015
 VERSION AB020755.1 GI:3985958
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 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 REFERENCE 1 Seto, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E., Kotani, H. and Tabata, S.
 STRUCTURAL ANALYSIS OF ARABIDOPSIS THALIANA CHROMOSOME 5. X.
 TITLE Sequence features of the regions of 3,076,755 bp covered by sixty p1 and TAC clones
 JOURNAL DNA Res. 7 (1), 31-63 (2000)
 PUBMED 10718197
 AUTHORS 2 (bases 1 to 81672)
 JOURNAL Nakamura, Y.
 TITLE Submitted (03-DEC-1998) Yasukazu Nakamura, Kazusa DNA Research
 REFERENCE Institute, Department of Plant Gene Research, 1532-3, Yana,
 JOURNAL Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp,
 COMMENT Tel:81-438-52-3335, Fax:81-438-52-3334)
 Address for correspondence: kaos@kazusa.or.jp
 For the latest information on annotation of this clone, please see
 http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c-MZNI
 Genes with similarity to proteins in the databases are described in
 'product' or 'note' qualifiers. Genes that have no significant
 protein similarity are described as 'unknown protein'.
 The software programs used to predict genes include: Grail
 (Informatics Group, Oak Ridge National Laboratory,
 http://compbio.ornl.gov/Grail-1.3/).
 GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
 NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
 Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
 SplicePredictor (Volker Brendel, Stanford University,
 http://gremlim.zool.iastate.edu/cgi-bin/sp.cgi).
 Genes encoding tRNAs are predicted by tRNAscan-SE
 (Sean Eddy, Washington University School of Medicine, St. Louis,
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CDS

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 16, 2006, 15:57:46 ; Search time 8511 Seconds
(without alignments)
5997.498 Million cell updates/sec

Title: US-10-634-548-1

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_eest1:*

2: gb_eest2:*

3: gb_eest3:*

4: gb_eest4:*

5: gb_eest5:*

6: gb_eest6:*

7: gb_eest7:*

8: gb_eest8:*

9: gb_eest9:*

10: gb_eest10:*

11: gb_eest11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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18	232.4	21.3	788	10	CL508895 SAIL.804
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ALIGNMENTS

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DEFINITION AU236980 RAPL15 Arabidopsis thaliana cDNA clone RAPL15-38-N13 5',
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ACCESSION AU236980
VERSION AU236980.1 GI:19876149
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS
Aktiyama, K., Enju, A., Oono, Y., Sakurai, T., Carminci, P., Kawai, J.,
Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinozaki, K.,
Muramatsu, M., Hayashizaki, Y., and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: meki@rc.riken.go.jp

TITLE
JOURNAL
COMMENT

as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FIC-1 vector (Carminci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified Bluescript vector. Please visit our web
site (http://www.gen.riken.go.jp/e/plant/index_e.html) for further
details.

FEATURES

SOURCE

location/Qualifiers
1..636
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAPL15-38-N13"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAPL15"
/notes="Site_1: BamHI; Site_2: SalI"

ORIGIN

FEATURES
source

Location/Qualifiers
1..864
/organism="Aquilegia formosa x Aquilegia pubescens"
/mol_type="mRNA"
/db_xref="taxon:338618"
/clone="COL102"
/tissue_type="mixed shoot and floral apical meristems,
flower buds, leaves and roots"
/lab_host="DH10B T1 (T1 and T5 phage resistance)"
/clone_lib="Aguilegia cDNA library"
/note="Vector: pCMV SPORT6.1; Site 1: EcoRI, Site 2: NotI;
F2, F3, and F4 lines of Aquilegia formosa x A. pubescens
were grown from seed in greenhouses at UC Santa Barbara.
From these plants three sets of tissue were collected: 1)
Small flower buds (<10 mm) and very young inflorescences
(71 & 29% by weight respectively), 2) Medium (7-20 mm) and
large (at or near anthesis) flower buds (65 & 35% by
weight respectively) and 3) Shoot apical meristems. A
fourth set of tissue was collected from plants of A.
formosa. These plants were grown from seed in sand and at
approximately 1 month root tissue and leaf tissue of
various developmental stages were collected (84 & 16% by
weight respectively). Total RNA was extracted from each
set of tissue and pooled in the following proportions:
1.5X from sets 1 & 2, 1X from sets 3 & 4. From the pooled
total RNA, mRNA was extracted and enriched for full-length
messages and then normalized with proprietary methods by
Invitrogen."

ORIGIN

Query Match 28.8%; Score 313.8; DB 8; Length 864;
Best Local Similarity 64.9%; Pred. No. 1e-76;
Matches 465; Conservative 0; Mismatches 252; Indels 0; Gaps 0;

304 CGCTGTCAGAGAGTCGAGACCCGTCGAGCTTGTGGAGCATACCCGCTGTCT 363
Db CACTTGGCAGAGTCAGAGTCGAGCGGACCTGTAGTGGTGGCCATCGTCTTGTAC 732
364 TAAAGCTTCAGAGTCCTCAAGCGAAGCTCATTCACAGAGTTTGAGCAAGAGCTTG 423
Db GTTCTTGTAGATCTTCTAGAGAGGATTTATCAACAGAGTTTGAGCAAGAGAGTGG 672
424 TGCATATATCTCAAGTCGTCTTGTCTGACTTGGCGGCAATCTTCAGCGAATCGACCG 483
Db TTCAATATGTCTGGGCTCTATTCATGCTTCTTGGCAATTTTATGTAATCAACCG 612
484 AGGCTCATATCTTGTCTTGTCCGTAGTGAAGAGGCTTAAAGCTTGTATTAAAG 543
Db AAGCTCGTACTTGGTCGATTTGCTCTTTGAATGTGAGAGCTTGTCTCTCAATG 552
544 GACTATCATTTCCCAATTCAGATGTAATCAATCCGTCAAGAGAGAGAGAGAG 603
Db GACTTTCATGACGATGATAGAGGTCTTGTGAATCTGTCAACAGTGAAGAGAAATCCA 492
604 AAGAGTTCCTTAAAGTCTTGTCTTGAAGCTCTTCTTCTGCGGCTTTCT 663
Db AGGAATCTCTGAGAGTCTCTCTACTGATGTTTAAATGTGATGCCAGTCAATAT 432
664 TCTGAGAGAGTCTCTCTGATGATCTGTTAGCAATATGTGTGTGGCCATGAGAA 723
Db TCTGCGGTGAGTCTTCAAGTTGGAGATTGCACTAGCATATATGTGTGGAGATGTT 372
724 TAGCTGATATATAGGAGCTAAGTTGGGCACTTAAGATCTTCAACACCAAGAAAGA 783
Db TTGCTGATATCATTTGAGAAAGATTTGGGTCAATGATCCCATATATCAACAAAGA 312
784 GTTGGCAGAGAGATCTCAATGTTCAATCTTGGCTTTCATCTCAATGCAATTAATCTT 843
Db GTTATAGTGAAGTCTTCAATGTTTCAATTTGTTCTTGTGTCATTCATGATTTGCTAT 252
844 ACTATATCTCAAGCTTGGGATCTTCAATGATCTGGAAGAGCACTTTCAGAGAGATG 903
Db ACTATTTTTCAGCTCTTGGATTTTTCATATGGAAGTGTGATCTACAGTGGAGAAAGTGG 192

904 CAATGTCATATGTCGCGCAGGTAGTCAGTCGATACCCATCAACGATCAATTAGACG 963
Db CTTTAGAGCTTGTGGCAACATAGTAGAGTCCCTTCTACTACAGAGATAGTATAG 132
964 ACAATATTTGGTTCCTCTGCGTCACTATTTTACTGCTTATTTAAAGTTTGGATAT 1020
Db ACAACATTAAGTTCATTCATTCAGAGCAATGCTAATGGAATTAATGTTTCAAGCTAT 75

RESULT 8

CK286787 881 bp mRNA linear EST 02-AUG-2004
LOCUS EST749509 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBM462.5'

end, mRNA sequence.
CK286787
ACCESSION CK286787.1 GI:39862689

VERSION
KEYWORDS
SOURCE
ORGANISM

Nicotiana benthamiana
Nicotiana benthamiana
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 881)
Buell, C.R., Hart, A., Zismann, V., Karameycheva, S.A., Day, B.,
Staskiewicz, B., Jin, H., and Baker, B.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Other ESTs: EST749510
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
Clones can be requested from the University of Arizona Genomics
Institute via <http://genome.arizona.edu/orders/>.
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
source

Location/Qualifiers
1..881
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBM462"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-TonA"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI, Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomla 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Query Match 28.2%; Score 307.8; DB 7; Length 881;
Best Local Similarity 67.2%; Pred. No. 5e-75;
Matches 435; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

303 TCGCTGTGATGACGTCGAGACCAAGTCGATGCTGTGGAGCATACGCGCTGTC 362
Db TCAAGTCGAGAGATGCGGAGGACCAAGCTTGTCTATCGCTGTGTGTTAGCCCTTGT 294
363 TTAAGCTTCAGAGTCTCAAGCGAAGCTCATTCACAGAGTTTGAGCAAGAGCTT 422
Db TCACTTTCAGATTTCTTATTCGAGCGCAAGCTCATTCAGAGATTTAAGCAAGAGCTT 354

Oy	443	GGCATAATATCTCAGAGTGTGCTTTTCGTACTTGCTGGCCAAATCTTGACGGATGAAAC	482
Db	355	GTCCACATATGTCTGTGTCTGCTTTTAATGCGTTCCTGGCCAAATTTTCAAGTCATCAAA	414
Oy	483	CAGGCTCGAATCTTTTGCTGCTTTTGTTCCTGTAGTAATGCTTAAAGCTTGTATTAAAC	542
Db	415	TGGGCAACGCTACCTTGCTCTGTAGTTCCGCTTCAACAACTGTTTGACCTTGATTTAT	474
Oy	543	GGACTATCCATTTCCCAAAATTCAGATGCTAAATCCGTCAACAGAGGAGAGAGA	602
Db	475	GGCCTTTCTTTTGGCTAAGTATGAGGACCTTCTTAAATCTGTTAAGTGGAGAGAAACCA	534
Oy	603	GAAAGTTGCTTAAAGTCTCTTGTTCATAGTTCTTACCTCTCTTTCTCTGGGTTTTTC	662
Db	535	GAAAGATTGCTTAAAGGGGCTCTAATATATATGTTAGTCTTAAATTTTGAACCCACCTTCTC	594
Oy	663	TTCTGAGAGAGTCTCCTTACGGTATGATCTGTAGCAATGATGTGTGGTGGCCATGGA	722
Db	555	TTTTTGCGGAGTCAACCAATTGGAATATTTGCTTAGCAATATATGTGTGTGTATGGA	654
Oy	723	ATAGCTGATATATAGGGAAGTAAAGTTTGGGTCACTAAGATACCTTCAACCCAGAAAG	782
Db	655	ATTGCTGATATTTGGAAAGAGTTTGGGTCCATATAAATCCCTTATATATTAACAGAA	714
Oy	783	AGTTGGGACGAAAGCATCCCATGTTCACTTCCGCTTTCATCTCCATCCATTACT	842
Db	715	AGTTTGGCGTGAAGCTCTCCATATGTTTGTCTTGCGTTTCTGTGTCCATTTGGATGCTC	774
Oy	843	TACTATTACTCAAGCCTTGGGATACCTTCAATGAACGTGGAAAACGACTTGCAGAGAGTA	902
Db	775	TATTACTTCTCGTCCCTTGGGATATCTTCACTTGGAATGGGTTTCAACGTATAAAAGTGA	834
Oy	903	GCAATGCTCAATGTCGCCACGGTACAGTCCAGTCCATCCATCAC	949
Db	835	GGTGTGTGTCAATTAATAGCACTAATGATGGAGTCTTAACTTAATAC	881

FEATURES	source
LOCUS	CA297624/c
DEFINITION	CA297624
ACCESSION	SCCCSDC02H02.g SD2 Saccharum officinarum cDNA clone SCCCSDC02H02
VERSION	CA297624
KEYWORDS	5' mRNA sequence.
SOURCE	CA297624.1 GI:36066481
ORGANISM	EST. Saccharum officinarum Saccharum officinarum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogonaceae; Saccharum; Saccharum officinarum complex. 1 (bases 1 to 787) Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P. The 11barries that made SUCESR Genet. Mol. Biol. 24 (1-4), 1-7 (2001) Contact: Arruda P Centro de Biologia Molecular e Engenharia Genetica Universidade Estadual de Campinas Caixa Postal 6010, 13083-970, Campinas SP, Brazil Tel: 55 19 3788 1137 Fax: 55 19 3788 1089 Email: paruda@unicamp.br Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br plate: C02 row: H column: 02 Seq primer: T7 Promoter Primer. Location/Qualifiers 1..787

FEATURES	SOURCE	location/qualifiers
		1..787
		/organism="Saccharum officinarum"
		/mol_type="mRNA"
		/db_xref="taxon:4547"
		/clone="SCCSD2C02H02"

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/1ab host="PH10B"
/clone lib="SD2"
/notes="Organ: Developing seeds (small insert library);
Vector: pSPort1; Site 1: SalI; Site 2: NotI; An
unidirectional cDNA library generated from [Developing
seeds (small insert library)]. cDNA was prepared from
polya+ mRNA using Superscript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucsec.tad.ic.unicamp.br/publi4c"

```

	Query Match	Best Local Similarity	25.6%; Score 278.8; DB 6; Length 787;	
		63.0%; Pred. No. 7.1e-67;		
	Matches	430; Conservative	0; Mismatches 255; Indels	0; Gaps
QY	324	GCCACCGGTGGAGGCTTGTTGGAGCATGCGCTTGTCTTAAGCTTGAGAGTCTACG	383	
DB	779	GTCAAGGTGCTCATCATCTGTGGGCGCATCTCTTTTGGCGGTCTTGACGAGCTCAC	720	
QY	384	AAGGAAAGCTCATTTCAACAGAGTTTGAAGGAAAGCTTGTGCATATATCTCAGAGTCG	443	
DB	719	GAGGGGCGCTCATCGAAMAGATTGAGCAGGAAGCTGTGCAGATGCTATCTAGCGCTC	660	
QY	444	CTTTTCGACTTGGGTGGCCAAATCTTGACGGATCGACCGAGGCTGCATATCTTCTGCT	503	
DB	659	CTGTTCATGTTCATCTTGGCCACTGTTCAGTAATTCGACAGAAAGCAGGTAATTTCCGCGCA	600	
QY	504	TTTGTTCGCTTGAAGATGAGCTTAAGCTTGTATTAACGAGTATTCATTTCCCAAT	563	
DB	599	GTGTTCATTCATTTGAAGCTCATTAAGGTTTGTGACATACGAGCTCGGCTGCACATGAT	540	
QY	564	TGCATGCTAATCAAAATCCGTCAACAAGAGGAGAGCAGAAAGATTGCTTAAAGTCT	623	
DB	539	GAACTCTAGTAATAATCAGTACACGTGAGAAAGAAACAGAGGATTACTGAGAGTCCA	480	
QY	624	TTTGTTCAGCTTGAAGCTCTTCTTCTCTGCGGTTTCTCTGAGAGAGCTCTCATAC	683	
DB	479	CTTATTAATGTCTTGGTGTCTGTCTTCAAGTATTTAGTCTTCTTGGCGAGTCCCCATT	420	
QY	684	GGTATGATCTCTGTAGCAATGATGTGTGTGGCGCATGATAGCTGATATATAGGAGCT	743	
DB	419	GGGATGTGATCTTGTGATGATAGAGTGTGGCATGTGTTTGTGACATTTGTGGAGA	360	
QY	744	AAGTTTGGGTCACTAAGATACCTTACACCCAAAGAAAGATTGGGCAAGAACATCTCC	803	
DB	359	AGTATGAGCTCAGGAAGCTGCCAATTCATGAGAAAGATGTGGGCGGAAAGCATCTCT	300	
QY	804	ATGTTCATCTTGGCTCTTTCATCTCCATGSCATTAATCTTACTTACTCAAGCCTGGG	863	
DB	299	ATGTTCAATTTCTGATTTTCTGTCTGTCTGTGCGATGATGATGTTCTTCAAGCCTGGGT	240	
QY	864	TACCTTCAATGAACTGGGAAACGACTTGGCAGAGATGAGCAATGTCTCAATGTGCGC	923	
DB	239	TACATTCATGTATCTGTGGAGAGGACACTCGGTAGCTGGGCTTGTGTGCACTGGCAGA	180	
QY	924	ACGGTACGTGAGTGCCTAACCCATCAACGATCAATTAGACGAATATTTGGTTCCTCG	983	
DB	179	ACAGTATGTGAGTGCATTTCTGTGACTGAAAGTTGATGATGACAAATATATCTGTTTG	120	
QY	984	GCTACTATTTTAACTGCTATATT	1006	
DB	119	GCCACCAAGCTGTAGCTTTTCT	97	

RESULT 10	LOCUS	DEFINITION
BG412580	BG412580	654 bp mRNA linear EST 13-MAR-2001
OV2_3611.g1_A002	OV2_3611.g1_A002	Ovary 2 (OV2) Sorghum bicolor CDNA, mRNA sequence.

ACCESSION BG412580
 VERSION BG412580.1 GI:13318133
 KEYWORDS EST.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Sorghum.
 REFERENCE 1 (bases 1 to 654)
 Cordonier-Pratt, M.-W., Gingle, A., Marsala, C., Sudman, M. and Prict, L.H.
 TITLE An EST database from Sorghum: ovaries of varying immature stages
 JOURNAL Unpublished (2000)
 COMMENT Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmprratt@uga.edu
 Seq primer: PolYTmX
 High quality sequence start: 8
 High quality sequence stop: 628
 POLYA=No.

FEATURES
 source
 1..654
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /clone_lib="Ovary 2 (OV2)"
 /note="Organ: Mix of ovaries of varying immature stages from 8-week-old plants; Vector: pluscript II from lambda zap II; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda zap II. Clones to be sequenced were prepared by mass excision."

ORIGIN
 Query Match 24.3%; Score 265.6; DB 2; Length 654;
 Best Local Similarity 64.1%; Pred. No. 3.5e-63;
 Matches 400; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

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Oy 368 CTTCGAGAGTCTACCAAGCAAGAGTATTCACAGAGTTGAGCAGAAAGCTTGCA 427
    |||||
Db 3 CTTCGAGAGTCTACCAAGCAAGAGTATTCACAGAGTTGAGCAGAAAGCTTGCA 62
    |||||
Oy 428 TATCTCTCAGTCTGCTTTCGTACTGCGGCGCAATCTTCAGCGGATGACCGAGGC 487
    |||||
Db 63 CGTGTATTCGCGCGCTCTGTTCATGTCACTTGGCGCTGTTCAAGCAATTCAGCAGAGC 122
    |||||
Oy 488 TCGATACTTTCGCTGTTTGTTCGCTTAGTGAATGGCTTAAGCTTGTATTAACGACT 547
    |||||
Db 123 ACGGATATTCGCTGAGTTGTTCCACTCTTGAACCTCAATAGGCTTGTATTAAGACT 182
    |||||
Oy 548 ATTCATTTCCCAATTGATGCTATCAAAATCCGTCACAGAGAGGAGAGCAGAGA 607
    |||||
Db 183 CCGTCTCTACACTGATGAAGCTCTAGTAAATCACTGACACGTGAAGGAAAAACAGAGA 242
    |||||
Oy 608 GTTGTAAAGGCTTGTGTTCTAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTG 667
    |||||
Db 243 ATTGCTGAGAGGCTCAGTATTAATGTTGCTGCTGTTGCTGCTGTTGCTGTTGCTG 302
    |||||
Oy 668 GAGAGAGTCTCTATCGGTATGATCTCGTTAGCAATGATGTGTGCGATGAGATAGC 727
    |||||
Db 303 GCGGAGAGTCCCTGTTGGGATGTTCTCTTTGTCATGATGATGATGATGATGATG 362
    |||||
Oy 728 TGATTAATGGAGCTTAAGTTGGGTCACTAAGATACCTTAACCAAGAGAGATTG 787
    |||||
Db 363 TGACATTTGTGGGAGAGATGAGCTCAGTGAAGCTGCAATTCATTAAGAGAGCTG 422
    |||||
Oy 788 GGCAGAGAGCATCTCATGTTGATCTTGCGGCTTTCATCTCCATCGCATTAATTA 847
    |||||
Db 423 GCGCGGAGCATCTCATGTTGATCTTGCGGCTTTCATCTCCATCGCATTAATTA 482
    |||||

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Oy 848 TTACTCAAGCTTGGGTACTTCATGAACTGGGAGAAAGCACTTGACAGAGTACCAAT 907
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 Db 483 CTTCGAGAGCTTGGTTACATGATGTTATTTGGCAGAGGCACTTGTAAGCGCGCT 542
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 Oy 908 GGTCTCAATGGTCCACCGGTAGTCAGTCCATACCATCAAGCATTAAGACGACAA 967
 |||||
 Db 543 TGTTCACCTGGCAGCAACCGTATGAGATGATTCCTGTACATGAACTTGAATGACAA 602
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 Oy 968 TATTCGCTTCCTGCTGCTACTAT 991
 |||||
 Db 603 TATATCTGTTCTTGGCACCACAT 626
 |||||

RESULT 11
 DN207999/c
 LOCUS 734 bp mRNA linear EST 28-FEB-2005
 DEFINITION MEST64_B02.T7-1 UGA-ZMSAM-XZ2 Zea mays cDNA, mRNA sequence.
 ACCESSION DN207999
 VERSION DN207999.1 GI:60341026
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE
 AUTHORS Chen, H.D., Zhang, X., Zhou, R.L., Arias, L.A.C., Shendelman, J.M., Zazubovics, N., Boreuk, L.A., Emrich, S.J., Ashlock, D.A., Scanlon, M.J. and Schnable, P.S.
 TITLE Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
 JOURNAL Unpublished (2004)
 COMMENT Contact: Patrick S. Schnable
 Schnable Laboratory
 Iowa State University
 2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
 Tel: 515-294-0975
 Fax: 515-294-5256
 Email: schnable@iastate.edu.

FEATURES
 source
 1..734
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="Indred B73"
 /db_xref="taxon:4577"
 /tissue_type="Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4"
 /lab_host="XJ1-Blue"
 /clone_lib="UGA-ZMSAM-XZ2"

/note="Organ: Shoot apex; Vector: Uni-Zap XR; Site 1: EcoRI; Site 2: XhoI; This library was constructed by Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4 from 14-17 day-after germination seedlings were quickly dissected into dry ice under a light microscope. Total RNA was isolated using Trizol and mRNA was purified with Dynal Oligo-dT25. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer
 (5'-GAGAGAGAGAGAGAGAGACTGCTGAGTTTCTTTTCTTTT).
 The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptor, the ds-cDNAs were digested with XhoI and size-selected to be >600 bp. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the Uni-Zap XR vector. The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by X1-blue cells and ExSatis helper phage. Excised phagemids were titered in SOLR cells and plated onto LB-ampicillin agar plates. Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria:
 (-minimum 200-error 0.01 0.01-bracket 10 0.01). A low complexity filter was applied and additional trimming was

conducted to remove *B. coli* vector, and organelle contamination. After processing ~10% of the sequences contained a minimum of 10 Ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."

ORIGIN

Query Match 24.2%; Score 264.2; DB 8; Length 734;
 Best Local Similarity 63.8%; Pred. No. 9e-63;
 Matches 401; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

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Qy 378 CTCACCAAGCGAAAGCTATTCACAGAGTTGAGCAGAAAGCTGTGATATCTCA 437
Db 728 CTCACCGAGCGCGGCTCATGAAAAGCTTGAGCAGAAAGCTGTGATCTCC 669
Qy 438 GGTCTGCTTTTCTGATCTTGCGGCAATCTTCAGCGGATCGACGAGCTCTATCTT 497
Db 668 GGGCTCTGCTCATGTCATCTTGCCCTGTTGAGCAATTCGACAGAGCAAGGATTTTC 609
Qy 498 GCTGCTTTTGTCCGTTAGTGAATGCTTAAAGCTTGTATTAACGACTATCCATTTCC 557
Db 608 GCCCGGTTGTCGGCTTCTAACTCAATGAGGCTTCTGATATATGAGCTCCGCTCTAC 549
Qy 558 CCAATTCGATGCTAATCAATCCGTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 617
Db 548 ACTGATGAGCTCTGTTAAATCACTGACAGTGAAGAAAACAGAGAAATGCTGAGA 489
Qy 618 GGTCTTTTCTGATCTGATCTGCTTTCTTCTGCGGTTTCTTCTGAGAGAGTCT 677
Db 488 GGTCTCACTATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 429
Qy 678 CTTATCGGTATGATCTGTTAGCAATGATGTTGTTGTTGTTGTTGTTGTTGTTGTT 737
Db 428 CCCATCGGAGCTGCTCTCTTCTGATGATGAGCGGTGCGAGTGTGCTGACATGTT 369
Qy 738 GAGAGTATGTTGGGTCACTAAGATACCTTACCAACCAAGAGAGTGGGAGAGAG 797
Db 368 GGGAGAGATATGCTGACGAGAGCTGCAATTCAGAGAGAGAGAGAGAGAGAGAG 309
Qy 798 ATCTCATGTTTCTGCTGCTTCTTCTGATCTGATCTGATCTTATCTTATCTCAAG 857
Db 308 ATCTCATGTTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 249
Qy 858 CTGGGATCTTCACTCAATCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 917
Db 248 CTGGGATCAATGATGATGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 189
Qy 918 GTGCGCAGGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 977
Db 188 GAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 129
Qy 978 CTTCTGCTACTATTTTATGCTGTTATTT 1006
Db 128 CTTTGGCAGCAGAGCTGAGCTTTTCT 100

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RESULT 12
 CV711742/c 883 bp mRNA 1linear EST 03-NOV-2004
 LOCUS UCRPT01.001605.f Poncirus trifoliata CTV-challenged cDNA library -
 DEFINITION AG12 Poncirus trifoliata cDNA clone PT_68A001605, mRNA sequence.
 ACCESSION CV711742
 VERSION CV711742.1 GI:55294110
 KEYWORDS EST.
 SOURCE Poncirus trifoliata
 ORGANISM Poncirus trifoliata
 Bacteria: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Sapindales; Rutaceae; Poncirus.
 1 (bases 1 to 883)
 Rose, M.L., Ye, X., Federici, C.F., Close, T.J., Fenton, R.D.,
 Manamaker, S., Kim, H.R., Kudrna, D. and Stum, D., Wiscotski, M.,

TITLE
 JOURNAL
 COMMENT
 Ming, R.
 Development of EST Resources and New Genetic Markers for California
 Citrus - Poncirus trifoliata CTV-challenged phloem - AG12
 Unpublished (2004)
 Contact: Mikeal Rose
 Department of Botany & Plant Sciences, University of California
 Riverside, CA, 92521-0124, USA
 Tel: 9097874437
 Fax: 9097874437
 Email: mikeal.rose@ucr.edu
 Seq primer: T7.

FEATURES

source

Location/Qualifiers

1..883

/organism="Poncirus trifoliata"

/mol_type="mRNA"

/cultivar="Pomeroxy OP"

/db_xref="taxon:37630"

/clone="PT_68A001605"

/tissue_type="phloem"

/dev_stage="10 - 30 cm shoots"

/lab_host="B. coli TUC121"

/clone_id="Poncirus trifoliata CTV-challenged cDNA library - AG12"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
 Site 1: EcoRI, Site 2: XhoI; plants were grown in the
 greenhouse at University of California, Riverside. The
 section was an open-pollinated (very probably selfed)
 seedling of Poncirus trifoliata cv Pomeroxy that was
 selected as homozygous for the CTV resistance gene. The
 rootstock was sweet orange infected with citrus tristeza
 virus (CTV) isolate T514 over 1 year before sampling (CTV
 infects sweet orange, but not genotypes carrying the CTV
 resistance gene). Shoots 10-30 cm long were harvested in
 October 2000, and the green phloem (dark) was removed and
 frozen quickly in dry ice. Total RNA was extracted using
 TRIzol reagent (Gibco). Poly(A) RNA was purified, a cDNA
 library was made, and 0.5 million primary lambda cDNA
 clones were in vivo excised to give a population of
 phagescript SK(-) phagemids. All steps to this point were
 performed in the ML Rose lab at the University of
 California, Riverside by X. Ye. Phagemids were plated,
 plasmid DNA purified, cDNA clones archived, and DNA
 sequences determined bi-directionally using an ABI3730 at
 the Arizona Genomics Institute, University of Arizona
 (Kim, Kudrna, Stum, Wiscotski, Ming). Chromatogram files
 were downloaded to UC Riverside (Close), then processed at
 UC Riverside (Manamaker) using the HarveST pipeline
 (http://harvest.ucr.edu) to remove vector and cloning
 oligo sequences and various contaminants, and to trim to a
 high quality region. Sequences that retained a phred 17
 region of at least 100 bases were deposited to Genbank."

ORIGIN

Query Match 23.5%; Score 256.4; DB 7; Length 883;
 Best Local Similarity 66.0%; Pred. No. 1.5e-60;
 Matches 371; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

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Qy 471 AGCGATGACCGAGGCTGATCTTGTGCTTTTGTCCGTAGTGAATGCTTAAG 530
Db 703 AGCAGCTCAACAGAGGCTGCTACTTGTGCGCTTGTCTCTGTGAATGCTTGA 644
Qy 531 CTGTGTTTAAAGGATCTATCTATTTCCCAATTCATGCTATCAATCCGTCACAGA 590
Db 643 CTGTGTTTAAAGGCTCTCATTAAGTAAGAGAGAGAGAGAGAGAGAGAGAGAG 584
Qy 591 GAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 650
Db 583 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 524
Qy 651 TCTGCGGTTTCTTCTGAGAGAGTCTCTATCGGTATGATCTGTTAGCAATGATGT 710
Db 523 TCTGCTCTGCTTTTGGCGTGAATGCCAGTGTGGGATGATCTCTCGATGATGTGT 464

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QY 711 GGTGGCATGATAGTGAATATATATAGGAGCTAGTTGGGTCACTAGATACCTTAC 770
 Db 463 GGGGAGATGCTGTGTCTGACGTTATGGAAGAAATTTGGGTCCATGAAAGATCTTTAT 404
 QY 771 AACCAAGAAAGATGGGCGAGAAAGCATCTCCATGTTTCATCTTCCGCTTCTCATCTCC 830
 Db 403 AATAGAAAAAAGTTGGGTGGCGATATATCAATGTTTGGATCTTTCATGTTCC 344
 QY 831 ATGCAATACCTTCTTCTTATCTCAAGCCTTGGGTACCTTCATGATGAGAAAGACC 890
 Db 343 ATTGGATGCTGTAATCTTATTCATTTTGGATATTTACACTGATTTGATGAGACA 284
 QY 891 TTGCAGAGATGAGAAATGCTCATGCTGCGCACGATGATGAGTGCATCCATCACC 950
 Db 283 TTGCAGAGGCTTGTGTTTATGCTCTAGTGGCGACAGTGTGAGTCTCTCCGATTTACA 224
 QY 951 GATCAATTAGACGACATATTTGCGTTCTCTGCTACTATTTTACTGCTTATTTAAGT 1010
 Db 223 GAGCTTGATGATGACATATATCTGTTCTCTTCCAGACATGATGACATATTTGAGT 164
 QY 1011 TTGGATATTGATTAATCCCT 1032
 Db 163 TTGTTATTGATTTGATCTT 142

RESULT 13 675 bp mRNA linear EST 01-MAR-2005
 DN229569/c

LOCUS DN229569 F09.T7-1 UGA-ZmsAM-X22 Zea mays cDNA, mRNA sequence.

DEFINITION DN229569

ACCESSION DN229569

VERSION DN229569.1 GI:60396702

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Zea mays

AUTHORS Zea mays

TITLE Zea mays

JOURNAL Zea mays

COMMENT Zea mays

FEATURES Zea mays

SOURCE Zea mays

ORIGIN Zea mays

DEFINITION Zea mays

ACCESSION Zea mays

VERSION Zea mays

KEYWORDS Zea mays

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Zea mays

AUTHORS Zea mays

TITLE Zea mays

JOURNAL Zea mays

COMMENT Zea mays

FEATURES Zea mays

SOURCE Zea mays

synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected to be >600 bp. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the Uni-Zap XR vector. The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by Xli-Blue cells and Exsistist helper phage. Excised phagemids were titered in SOLR cells and plated onto LB-ampicillin agar plates. Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria: (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove E. coli, vector, and organelle contamination. After processing ~30% of the sequences contained a minimum of 10 Ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."

ORIGIN

Query Match 23.4%; Score 255; DB 8; Length 675;
 Best Local Similarity 63.8%; Pred. No. 3,4e-60;
 Matches 387; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

QY 400 AACAGATTGACGAGAAAGCTTGTGCAATATCTCAAGTCTGCTTTGTAAGTCCGT 459
 Db 672 AAAAGAGCTTACGACAGAAAGTTGTGCAAGTCTGATCCGCTCTGTCATGTCATCTT 613
 QY 460 GGGCAATCTTACCGGATTCGACGAGCTGATCTTGTGCTTTGTTCCGTTAGTGA 519
 Db 612 GGGCCCTGTTACGAAATTCGACAGAAAGCATGTTGCGCGCGTGTCCGTTCTGTA 553
 QY 520 ATGCTTAAAGCTTGTATTAAGCAATATCTATCCCAATTTCCATGCTAATCAAT 579
 Db 552 ACTCCATGAGAGCTTCTGATATATGAGACTCGGTCTTACATGATGAAAGCTGTGTAAT 493
 QY 580 CCGTCAAG 639
 Db 492 CAGTGAACAGCTGAAG 433
 QY 640 CT 699
 Db 432 TGTCTGTTTCAAGCTTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 373
 QY 700 CAATGATGTGTGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 759
 Db 372 CGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 313
 QY 760 AGATACCTTAACCAAG 819
 Db 312 AGCTGCATTCATTCGAG 253
 QY 820 TCTTCAATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 879
 Db 252 TCTGCTGTCTCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 193
 QY 880 GGAAG 939
 Db 192 GGAAG 133
 QY 940 TACCATCAGCATTAATTAAG 999
 Db 132 TTCTGTGACGAG 73
 QY 1000 CTTTATT 1006
 Db 72 CTTTCT 66

RESULT 14

CD405855/c 658 bp mRNA linear EST 07-JUN-2003
 LOCUS CD405855
 DEFINITION Gm_cx2937 Soybean induced by Salicylic Acid Glycine max cDNA 3',

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

CM nucleic - nucleic search, using sw model

Run on: March 16, 2006, 16:17:44 / Search time 646 Seconds
(without alignments)
3002.043 Million cell updates/sec

Title: US-10-634-548-1
Perfect score: 1091
Sequence: 1 aaaaagaataataataa.....ccgacctacaatgttcc 1091

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	67	6.1	7218	2	US-08-232-463-14
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8	39.4	3.6	524032	3	US-09-949-016-16928
9	39.4	3.6	524032	3	US-09-949-016-16929
10	39.4	3.6	524032	3	US-09-949-016-16930
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23	37.4	3.4	832	3	US-09-621-976-2813
24	37	3.4	435	3	US-09-252-991A-6687

25	37	3.4	32010	3	US-09-949-016-13127	Sequence 13127, A
26	36.8	3.4	3117	3	US-09-614-221A-275	Sequence 275, App
27	36.4	3.3	76401	3	US-09-949-016-17153	Sequence 17153, A
28	36	3.3	87780	3	US-09-949-016-17011	Sequence 17011, A
29	36	3.3	90428	3	US-09-949-016-12564	Sequence 12564, A
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31	36	3.3	152583	3	US-09-949-016-17306	Sequence 17306, A
32	36	3.3	152583	3	US-09-949-016-17301	Sequence 17301, A
33	35.8	3.3	288	3	US-09-313-294A-3968	Sequence 3968, App
34	35.8	3.3	601	3	US-09-328-111-530	Sequence 530, App
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37	35.6	3.3	601	3	US-09-949-016-17919	Sequence 17919, A
38	35.6	3.3	601	3	US-09-949-016-17920	Sequence 17920, A
39	35.6	3.3	601	3	US-09-949-016-11809	Sequence 41809, A
40	35.6	3.3	601	3	US-09-949-016-41810	Sequence 41810, A
41	35.6	3.3	2586	3	US-09-248-796A-1910	Sequence 1910, App
42	35.6	3.3	46841	3	US-09-949-016-13466	Sequence 13466, A
43	35.6	3.3	69813	3	US-09-949-016-12455	Sequence 12455, A
44	35.6	3.3	69813	3	US-09-949-016-13905	Sequence 13905, A
45	35.6	3.3	69813	3	US-09-949-016-13906	Sequence 13906, A

ALIGNMENTS

RESULT 1
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHRIFFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSES:
ADDRESSER: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpc-Fls

US-08-232-463-14

Query Match 6.1%; Score 67; DB 2; Length 7218;
 Best Local Similarity 2.5%; Pred. No. 7.5e-10;
 Matches 7; Conservative 187; Mismatches 87; Indels 0; Gaps 0;

[illegible]

RESULT 2

US-09-007-005-17/c
; Sequence 17, Application US/09007005B
; Patent No. 6258558

```

; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.

```

```

; APPLICANT: Liu, Rihé
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
;

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; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007, 005B
; CURRENT FILING DATE: 1998-01-14

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; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491

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; EARLIER FILING DATE: 1997-11-06
;
; NUMBER OF SEQ ID NOS: 33
;
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
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; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Translation template

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! FEATURE:
! NAME/KEY: misc_feature
! LOCATION: (1) ... (289)
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[illegible]

Oy 235 CCGAATGGGCTCTGCCTACTCAGTTACGTGTCGTCTCAKATCTCTTACG. 289
 : : : : : : : : : : : : | :
Db 101 YNYSNNYNSYNNNYSYNNNYSYNNNYSYNNNYSYNNNCYATTYYGY 47

RESULT 3

US-09-244-796-17/c
; Sequence 17, Application US/09244796

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; Patent No. 6281344
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.

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; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN

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; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350007
; CURRENT APPLICATION NUMBER: US/09/244,796

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; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27

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; EARLIER APPLICATION NUMBER: 60/064,491
;
; EARLIER FILING DATE: 1997-11-06
;
; EARLIER APPLICATION NUMBER: 09/007,005

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; EARLIER FILING DATE: 1998-01-14
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; NUMBER OF SEQ ID NOS: 33
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; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA

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; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Translation templates

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;; FEATURE:
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;; LOCATION: (1) ... (289)
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Oy	115	CACCTTACTCTACTCCGATCAATCATCACTGTGTGCGGTTCCGGAACAACCTTTTGA	174
Dd	221	YGSTNNYNYSNNYNYSNNYNYSNNYNYSNNYNYSNNYNYSNNYNYSNNYNYSN	162
Oy	175	GCACTCACCGGTTCTGTTCTCCTGCGCTTCTGATTCTTCTCCTTGTCATTGGTTGA	234
Dd	161	YNYSNNYNYSNNYNYSNNYNYSNNYNYSNNYNYSNNYNYSNNYNYSNNYNYSN	102
Oy	235	CCGGAATGGGCTCTGCTACTAGTTACGAGCTCGTCGTTCTGCACTCTTACG	289
Dd	101	YNYSNNYNYSNNYNYSNNYNYSNNYNYSNNYNYSNNYNYSNNYNYSNNYNYSN	47

RESULT 4

US-09-949-016-198946/c
; Sequence 198946, Application US/09949016

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; Patent No. 6812339
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; GENERAL INFORMATION:
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; APPLICANT: VENTER, J. Craig et al.

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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN
;
; TITLE OF INVENTION: WITH HUMAN DISEASE,
;
; FILE REFERENCE: CL001307

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;; CURRENT APPLICATION NUMBER: US/09/94
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 16, 2006, 18:40:51 ; Search time 3417 Seconds
(Without alignments)
2640.296 Million cell updates/sec

Title: US-10-634-548-1

Perfect score: 1091
Sequence: 1 aaaaaagaataatacaaa.....cgaactacaatgtttcc 1091

Scoring table: IDENTITY NUC
Gap 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	1091	100.0	1091	US-10-634-548-1	Sequence 1, Appl1
2	1015	93.0	1015	US-10-425-114-21028	Sequence 21028, A
3	977	89.6	980	US-10-425-114-14606	Sequence 14606, A
4	678.6	62.2	1062	US-10-425-114-29129	Sequence 29129, A
5	404	37.0	1897	US-10-634-548-3	Sequence 3, Appl1
6	337	30.9	1007	US-10-425-114-20410	Sequence 20410, A
7	294.6	27.0	1033	US-10-425-114-26593	Sequence 26593, A
8	294.6	27.0	1085	US-10-425-114-22326	Sequence 22326, A
9	294.6	27.0	1974	US-10-437-963-77301	Sequence 77301, A
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17	230.6	21.1	674	US-10-425-114-16877	Sequence 16877, A
18	187.4	17.2	516	US-10-424-599-54356	Sequence 54356, A
19	171	15.7	1091	US-10-425-114-26298	Sequence 26298, A
20	169	15.5	648	US-10-425-114-16929	Sequence 16929, A
21	169	15.5	666	US-10-425-114-4925	Sequence 4925, Ap
22	169	15.5	955	US-10-425-115-118754	Sequence 118754, A
23	167.2	15.3	688	US-10-425-114-22387	Sequence 22387, A

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27	161.6	14.8	1430	US-10-424-599-71025	Sequence 71025, A
28	160	14.7	1241	US-10-739-930-4866	Sequence 4866, Ap
29	155.8	14.3	795	US-10-425-114-13412	Sequence 13412, A
30	155.4	14.2	1225	US-10-425-114-26462	Sequence 26462, A
31	155.4	14.2	1286	US-10-425-115-172503	Sequence 172503, A
32	152.8	14.0	876	US-10-437-963-97687	Sequence 97687, A
33	147.2	13.5	944	US-10-425-114-19979	Sequence 19979, A
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37	144	13.2	948	US-10-435-114-19980	Sequence 19980, A
38	143	13.1	818	US-10-437-963-38063	Sequence 38063, A
39	143	13.1	1029	US-10-425-114-19799	Sequence 14899, A
40	141.4	13.0	1193	US-10-739-930-1297	Sequence 1297, Ap
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44	126	11.5	1044	US-10-425-114-26552	Sequence 26552, A
45	116.6	10.7	1057	US-10-767-701-11766	Sequence 11766, A

ALIGNMENTS

RESULT 1
US-10-634-548-1
Sequence 1, Application US/10634548
Publication No. US20040045051A1

GENERAL INFORMATION:

APPLICANT: No. US20040045051A1r1s, Susan R

APPLICANT: Lincoln, Kim

APPLICANT: Abad, Mark Scott

APPLICANT: Elfers, Robert

APPLICANT: Hartshuyker, Karen Kindle

APPLICANT: Hirschberg, Joseph

APPLICANT: Karunamadaa, Balasubramanian

APPLICANT: Moshiri, Farhad

APPLICANT: Stein, Joshua C.

APPLICANT: Valentini, Henry E.

APPLICANT: Venkatesh, Tyamagondlu V.

TITLE OR INVENTION: Tocopherol biosynthesis related genes and used thereof

FILE REFERENCE: Ren-01-125

CURRENT APPLICATION NUMBER: US/10/634,548

CURRENT FILING DATE: 2003-08-05

PRIOR APPLICATION NUMBER: us 60/400,689

PRIOR FILING DATE: 2002-08-05

NUMBER OF SEQ ID NOS: 79

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1

LENGTH: 1091

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-10-634-548-1

Query Match

Beat Local Similarity 100.0%; Pred. No. 5,5e-312;

Matches 1091, Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAAAAAGATTAATTAACAAATATCATTTCTTATATGACTGTCAAGATTCTCT	60
DB	1	AAAAAAGATTAATTAACAAATATCATTTCTTATATGACTGTCAAGATTCTCT	60
QY	61	TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	120
DB	61	TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	120
QY	121	TACCTTATCTCCGATCAATCAATGTTGTCGTTGCGGACAACTTTTGAAGATCTC	180
DB	121	TACCTTATCTCCGATCAATCAATGTTGTCGTTGCGGACAACTTTTGAAGATCTC	180

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QY 181 ACCGGTCTGTTCTCTGGCTTCTTGAATTCCTCTCTCTGTTTGAATGTTGAACCGGAA 240
DB 181 ACCGGTCTGTTCTCTGGCTTCTTGAATTCCTCTCTCTGTTTGAATGTTGAACCGGAA 240
QY 241 TGGGCTCTGCTACGATTAAGTGTGCTGCTGCTCTGATCTTTCAGCAAGTTCGACGA 300
DB 241 TGGGCTCTGCTACGATTAAGTGTGCTGCTGCTCTGATCTTTCAGCAAGTTCGACGA 300
QY 301 ATTGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 301 ATTGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 TCTTAAGCTTGAAGTCTCAACCAAGCAAGTCTTCAACCAAGTCTTCAACCAAGTCTTCA 420
DB 361 TCTTAAGCTTGAAGTCTCAACCAAGCAAGTCTTCAACCAAGTCTTCAACCAAGTCTTCA 420
QY 421 TTGTCATATATCTCTGAGTCTGCTTCTGATCTTCTGATCTTCTGATCTTCTGATCTTCT 480
DB 421 TTGTCATATATCTCTGAGTCTGCTTCTGATCTTCTGATCTTCTGATCTTCTGATCTTCT 480
QY 481 CCGAGGCTCGATATCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 540
DB 481 CCGAGGCTCGATATCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 540
QY 541 ACGGATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 600
DB 541 ACGGATATATATATATATATATATATATATATATATATATATATATATATATATATAT 600
QY 601 CAGAAAGTCTTAAAGTCTTCTTCTGATCTTCTGATCTTCTGATCTTCTGATCTTCTGATCT 660
DB 601 CAGAAAGTCTTAAAGTCTTCTTCTGATCTTCTGATCTTCTGATCTTCTGATCTTCTGATCT 660
QY 661 TCTTCTGAGAGAGTCTCTATCGGATGATCTGATGATGATGATGATGATGATGATGATGATG 720
DB 661 TCTTCTGAGAGAGTCTCTATCGGATGATCTGATGATGATGATGATGATGATGATGATGATG 720
QY 721 GAATAGCTGATATATATATATATATATATATATATATATATATATATATATATATATATAT 780
DB 721 GAATAGCTGATATATATATATATATATATATATATATATATATATATATATATATATATAT 780
QY 781 AGAGTTGGGCGAAGAGCTCTCCAGTCTTCAATCTTCCAGTCTTCAATCTTCCAGTCTTCA 840
DB 781 AGAGTTGGGCGAAGAGCTCTCCAGTCTTCAATCTTCCAGTCTTCAATCTTCCAGTCTTCA 840
QY 841 TTTTCTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 900
DB 841 TTTTCTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 900
QY 901 TAGCAATGATCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 901 TAGCAATGATCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 961 ACGACATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1020
DB 961 ACGACATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1020
QY 1021 AGATTAATCCCTCATTAACCGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 AGATTAATCCCTCATTAACCGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 CAATGATTTCC 1091
DB 1081 CAATGATTTCC 1091

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RESULT 2
US-10-425-114-21028
; Sequence 21028, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.

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; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT FILING DATE: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 21028
; LENGTH: 1015
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana columbia
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3278-077-DS_FLI
US-10-425-114-21028

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Query Match 93.0%; Score 1015; DB 7; Length 1015;
Best Local Similarity 100.0%; Pred. No. 1,7e-289; Mismatches 0; Gaps 0;
Matches 1015; Conservative 0; Indels 0;

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QY 74 CTTCTCTCTCTCCAACTGATGCTTCCCTGCTGATGATGATGATGATGATGATGATGATGAT 133
DB 1 CTTCTCTCTCTCCAACTGATGCTTCCCTGCTGATGATGATGATGATGATGATGATGATGAT 60
QY 134 GATCAATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 193
DB 61 GATCAATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
QY 194 TCTGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 253
DB 121 TCTGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 254 TCAATTAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 313
DB 181 TCAATTAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 314 TGAAGTGGAGCAACCGTGGAGTGTGAGAGCATACGCGCTTGTCTTAAGCTTGA 373
DB 241 TGAAGTGGAGCAACCGTGGAGTGTGAGAGCATACGCGCTTGTCTTAAGCTTGA 300
QY 374 GAGTCTCAACCAAGGAAAGCTTCAACCAAGGATGATGATGATGATGATGATGATGATGAT 433
DB 301 GAGTCTCAACCAAGGAAAGCTTCAACCAAGGATGATGATGATGATGATGATGATGATGAT 360
QY 434 CTGAGTCTGCTTCTGATCTTCTGATCTTCTGATCTTCTGATCTTCTGATCTTCTGATCTTCT 493
DB 361 CTGAGTCTGCTTCTGATCTTCTGATCTTCTGATCTTCTGATCTTCTGATCTTCTGATCTTCT 420
QY 494 CTTTCTGCTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 553
DB 421 CTTTCTGCTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 554 TTCCCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 613
DB 481 TTCCCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 614 TAAAGTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 673
DB 541 TAAAGTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
QY 674 GTCTCTATCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 733
DB 601 GTCTCTATCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 734 AATGAGAGTAAAGTGGGCTCACTAAGATCTTCAACCAAGGAAAGGATGGGCGAG 793
DB 661 AATGAGAGTAAAGTGGGCTCACTAAGATCTTCAACCAAGGAAAGGATGGGCGAG 720
QY 794 AAGCATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 853
DB 721 AAGCATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780

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QY 854 AACCTGGGATCTTCAATGAATCGGAAACGACCTTGCAGAGATGATGCTC 913
DB 781 AAGCTTGGATCTTCAATGAATCGGAAACGACCTTGCAGAGATGATGCTC 840
QY 914 AATGTCGCCACGGATGCTGCTACCCATCCATCAATTAATGAACAAATATTC 973
DB 841 AATGTCGCCACGGATGCTGCTACCCATCCATCAATTAATGAACAAATATTC 900
QY 974 GATTCCTGGATCTTCAATGAATCGGAAACGACCTTGCAGAGATGATGCTC 1033
DB 901 GATTCCTGGATCTTCAATGAATCGGAAACGACCTTGCAGAGATGATGCTC 960
QY 1034 ATAAACCGAATGTATATAGTATTTTATGAATCCGACCTTACAAATGTT 1088
DB 961 ATAAACCGAATGTATATAGTATTTTATGAATCCGACCTTACAAATGTT 1015

RESULT 3
US-10-425-114-14606
; Sequence 14606, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 14606
; LENGTH: 980
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; OTHER INFORMATION: Clone ID: LIB23-048-A2_FLI
US-10-425-114-14606

Query Match 89.6%; Score 977; DB 7; Length 980;
Best Local Similarity 100.0%; Pred. No. 3.1e-278; Indels 0; Gaps 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 CAACCTTACTTATCTCGATCATCATCATGTTGTCGTTGCGGAAACACTTTGA 174
DB 1 CAACCTTACTTATCTCGATCATCATCATGTTGTCGTTGCGGAAACACTTTGA 60
QY 175 CGACTCACCGGTTCTGTTCTCTGCTTCTGATTTCTTCTCTGTTTCAATGTTGA 234
DB 61 CGACTCACCGGTTCTGTTCTCTGCTTCTGATTTCTTCTCTGTTTCAATGTTGA 120
QY 235 CCGGAATGGGCTGCTACTAGTACGTCGTCGTTCTCTGATCTTCAAGAGTTG 294
DB 121 CCGGAATGGGCTGCTACTAGTACGTCGTCGTTCTCTGATCTTCAAGAGTTG 180
QY 295 CGAAGATTCGCTGTGATGACGTCGAGGCCGCTGCGAGTGTGTTGAGCATAG 354
DB 181 CGAAGATTCGCTGTGATGACGTCGAGGCCGCTGCGAGTGTGTTGAGCATAG 240
QY 355 CGCTTGTCTTAAGCTTCAAGAGTCTCACCAAGCGAAAGCTTCAACAGATTGACA 414
DB 241 CGCTTGTCTTAAGCTTCAAGAGTCTCACCAAGCGAAAGCTTCAACAGATTGACA 300
QY 415 GAAAGCTGTGATTAATCTCAAGTCTGCTTTTGTGTAATGCGGCAATCTCAGCG 474
DB 301 GAAAGCTGTGATTAATCTCAAGTCTGCTTTTGTGTAATGCGGCAATCTCAGCG 360
QY 475 GATGACCGAGGCTGATTAATGCTGCTTTTGTGTAATGCGGCAATCTCAGCG 534
DB 361 GATGACCGAGGCTGATTAATGCTGCTTTTGTGTAATGCGGCAATCTCAGCG 420

QY 535 TTATTAACGACATATTCATTTCCCAATTGATGATATGAATCCGTCAGAGAG 594
DB 421 TTATTAACGACATATTCATTTCCCAATTGATGATATGAATCCGTCAGAGAG 480
QY 595 GAGAGCAGAAAGTTGCTTAAGAGTCTTGTTCATAGTCTTACGTTCTTTCTCG 654
DB 481 GAGAGCAGAAAGTTGCTTAAGAGTCTTGTTCATAGTCTTACGTTCTTTCTCG 540
QY 655 CGTTTCTTCTGAGAGAGTCTCTATCGGTATGATCTGTTAGCAATGATGTGTTG 714
DB 541 CGTTTCTTCTGAGAGAGTCTCTATCGGTATGATCTGTTAGCAATGATGTGTTG 600
QY 715 GCGATGGAATGATGATTAATGAGAGTATGTTGGGTCAATAGATACCTTACAAC 774
DB 601 GCGATGGAATGATGATTAATGAGAGTATGTTGGGTCAATAGATACCTTACAAC 660
QY 775 CAAGAAAGATTTGGGAGAGAGATCTCCATGTTATCTTGGCTTCTCATCTCATCG 834
DB 661 CAAGAAAGATTTGGGAGAGAGATCTCCATGTTATCTTGGCTTCTCATCTCATCG 720
QY 835 CATTACTTACTTATTAATCAAGCTTGGGTACCTTACATGAATCTGGAAACGACTTGC 894
DB 721 CATTACTTACTTATTAATCAAGCTTGGGTACCTTACATGAATCTGGAAACGACTTGC 780
QY 895 AGAGATGACAAATGCTCATATGTCGCGACGATGATGATGCTTACCCATCACCGATC 954
DB 781 AGAGATGACAAATGCTCATATGTCGCGACGATGATGATGCTTACCCATCACCGATC 840
QY 955 AATTAGACGACAAATTTGCTTCTGCTGCTACTAATTTAGTCTTAAATGTTTCG 1014
DB 841 AATTAGACGACAAATTTGCTTCTGCTGCTACTAATTTAGTCTTAAATGTTTCG 900
QY 1015 GATATTAATTAATTCCTCATTAACCGAATGTATATGATTTTATGATTCG 1074
DB 901 GATATTAATTAATTCCTCATTAACCGAATGTATATGATTTTATGATTCG 960
QY 1075 ACCTTACAAATGTTTC 1091
DB 961 ACCTTACAAATGTTTC 977

RESULT 4
US-10-425-114-29129
; Sequence 29129, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 29129
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Brassica napus
; OTHER INFORMATION: Clone ID: LIB82-020-B9_FLI
US-10-425-114-29129

Query Match 62.2%; Score 678 6; DB 7; Length 1062;
Best Local Similarity 82.6%; Pred. No. 8.1e-190; Indels 0; Gaps 0;
Matches 777; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 108 ATGACAGCAACCTTACTTCTCCATCATCATGATGATGTTGCTGAGTCCGAGAACAC 167

ORGANISM: *Gossypium hirsutum*
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB3196-048-A11_FLI
 US-10-425-114-20410

Query Match 30.9%; Score 337; DB 7; Length 1007;
 Best Local Similarity 64.3%; Pred. No. 1.3e-88;
 Matches 505; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

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QY 280 TCTCTTCAAGCAGTTGCGAATTCGCTGTCATGACGTGAGCCGCTGGAGTGC 339
DB 181 TCTCAGCAGCCGCTGTAACCGCTCTATCTTCGAGATACCGCTCCCTCTCTCT 240
QY 340 TTGGTGAGCATACGCGCTGTTAAAGCTTCGAGCTTCACCAAGGAACGTCATTC 399
DB 241 TTGCTGGCGCTTAAGCTTCGCTTCACCTTCGATTCATTCACCAAGAGCTCATTC 300
QY 400 AACAGATTGAGAGAAAGCTTGATATCTCTAGCTCTGCTTTCCGTAATTCGCT 459
DB 301 AGCAGATTTAAGTAAGAAATGAGTATATATCTGATTCGATTCCTTTCCATTCCT 360
QY 460 GGCAGATCTTCAAGGATGACCAAGCTGATATCTTGTCTTTGCTTCCGTTAGTA 519
DB 361 GGCAGATTTTCAAGCAGCCGATGAGCTGTTACTTGTGATCTCTGCTTCACTTTCA 420
QY 520 ATGGCTTAAGCTGTTATTAACGATATCCATTCCTCCCAATTCATGATCAAAAT 579
DB 421 ATGCTTAAGCTGTTATTAAGTATCTCTCTTGAATGATGATCAAGCTTGAATCAAT 480
QY 580 CCGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 639
DB 481 CTGTTATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 640 CTCTTCTTTTCTGCGGCTTTCTTCTGAGAGAGTCTCTATGCTGATGATCTGTTAG 699
DB 541 TGTGATGATTAAGTCTCTGCTGTTGCTGCTGATATCCCGGAGGATCTGCTGCTGG 600
QY 700 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 759
DB 601 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 760 AGATACCTTACACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 819
DB 661 AGATTCCTTATATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 820 TCTTCATCTCCATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 879
DB 721 TCATCATTTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 880 GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 939
DB 781 GGGAGATATACCTCATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 940 TACCATCATACCATCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 999
DB 841 TTCCAAATTTCAATGATATGATATATATATATATATATATATATATATATATATATAT 900
QY 1000 CTATTTAAGTTGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1059
DB 901 CCAATTTAAGTTGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 960
QY 1060 TTTT 1064
DB 961 TTTT 965

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RESULT 7
 US-10-425-114-26593
 Sequence 26593, Application US/10425114
 Publication No. US20040034888A1
 GENERAL INFORMATION:
 APPLICANT: Liu, Jindong
 APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E
 APPLICANT: Tabaska, Jack E
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(5313)B
 CURRENT APPLICATION NUMBER: US/10/425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 26593
 LENGTH: 1033
 TYPE: DNA
 ORGANISM: *Oryza sativa*
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB4371-003-F9_FLI
 US-10-425-114-26593

Query Match 27.0%; Score 294.6; DB 7; Length 1033;
 Best Local Similarity 62.9%; Pred. No. 4.6e-76;
 Matches 456; Conservative 0; Mismatches 269; Indels 0; Gaps 0;

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QY 294 GCGAGAAATTCGCTGTCATGACGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 353
DB 192 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 251
QY 354 GCGCTTCTTAAGCTTCAAGAGTCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 413
DB 252 TCCCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 311
QY 414 AGAAGCTTGTGATATCTCTAGCTGCTGCTTTCGATCTTGGAGAGAGAGAGAGAGAGAG 473
DB 312 AGAAGATTTGATATGCTCTCGAGAGTCTGCTTCAATGCTTCTGAGAGAGAGAGAGAG 371
QY 474 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 533
DB 372 AATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
QY 534 GTTATTAAGAGATATATATATATATATATATATATATATATATATATATATATATAT 593
DB 432 CTGACCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
QY 594 GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 653
DB 492 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551
QY 654 GCGCTTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 713
DB 552 GTTTGATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 611
QY 714 GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 773
DB 612 GGTATGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 671
QY 774 CCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 833
DB 672 GAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 731
QY 834 GCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 893
DB 732 CTGATGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 791
QY 894 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 953
DB 792 GGTAACTGCTCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 851
QY 954 CAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1013
DB 852 GTTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 911
QY 1014 GAGATA 1018
DB 912 GGCTA 916

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Dd      860  GGTAAACGTGGCTCTTGTTGCATTAGACAGTACTGTAGTGGAGTATTTCTCGTCATATGAT  919
Qy      954  CAATTAGACGACAAATATTTCCGTTCCCTCTGCTACTATTTTACGTGTTATTTAAGTTTC  1013
          |||||
Dd      920  GTTGAGATGACAAATATCTCCGTTCTTGGCACCACATGTTGGCAGCCTATCTGTATTT  979
Qy      1014 GGATTA 1018
          ||||
Dd      980  GGCTTA 984

RESULT 9
US-10-437-963-77300
; Sequence 77300, Application US/10437963
; Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

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; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ. ID NOS: 204966
; SEQ. ID NO. 77300
; LENGTH: 1974
; TYPE: DNA
; ORGANISM: Oryza sativa
FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_77211C.1
US-10-437-963-77300

Query Match      27.0%; Score 294.6; DB 7; Length 1974;
Best Local Similarity 62.9%; Pred. No. 6,5e-76;
Matches 456; Conservative 0; Mismatches 269; Indels 0; Gaps 0;

Oy      294  GCGAGCAATTGCGCTTGTGATGACGTCGGAGCAACCGTGCCAAATGCTTGGTGGAGCAATAC 353
        |||||
Db      1224  GCGAGGCCCGCGGCGCTGCGGAGCACTGCGCGCCACCTGTCATACCGGCGGCGGTAC 1293
        |||||

Oy      354  GCGCTGTCTTAAAGCTTCGAGAGTCTCACCAAGCAAAAGCTCAATCAAGATTGAGC 413
        |||||
Db      1294  TCCCTGTGCGGCGCTTCGACGGGCTCACGGCGCGCGGTCTATCGAACAGAACTGAGC 1353
        |||||

Oy      414  AGAAAGCTTGTGCAATATACCTCAAGTCTGCTTTTGTACTTGCGTGCCAAATCTTCAGC 473
        |||||
Db      1354  AGAAATAATGTGCATATGCTCTCCGGAGTCCTGTATGTCCTTCTTGCCACTATTTCAGT 1413
        |||||

Oy      474  GGAATGACCGAGGCTCGAATACTTGTGCTTTGTCCTGCTAGGAATGGCTTAAAGCTT 533
        |||||
Db      1414  AATTCGACAGAGCAAGGCTTTCGCGCAATGTCCCGTGTGGAACCTGCATTAAGGCTT 1473
        |||||

Oy      534  GTTATTAAAGGACTATCACTTTCGCCAAATTCGATGCTAATCAATCCGTCAAGAGAA 593
        |||||
Db      1474  CTGACTATAGGGCTCCGCTTTCACACTGATGAAGCTCTAATAAATGGGTGACCCGTGA 1533
        |||||

Oy      594  GGGAGAGCAGAAAGAGTGTCTTAAAGTCTTTGTCTACGTTCTAGCTCTTCTTTCTCT 653
        |||||
Db      1534  GGAAACAACAGAGAAATGTCTGAGAGGTCTCTGTACTATGTCAATTGTGCTGCTGTCAGT 1593
        |||||

Oy      654  GCGGTTTCTTCTGGAGAGAGTCTCTATTCGATGATCTTCGTTAGCAATGATGTGGGT 713
        |||||
Db      1594  GTTTTGTCTTCTGGCGCAGTCTCTTATTTGGATGTTCCTGTTGTGATGATAGTGGT 1653
        |||||

Oy      714  GGCAGTGAATAGCTGATTAATATGGAGCGTAATTGGGTCAACTAAGATCACTTACAAC 773
        |||||
Db      1654  GGTGATGCGCTTGTCTGACATTTGTGGAGAAAGTATGTCTCCGGAAGCTCCCATTCAT 1713
        |||||

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Oy	594	GGAGAGAGAAAGTTGGCTTAAAGTCCCTTGTTCACGTTCAAGCTCTCTTCTCT	653
Db	1972	GGAAACCAAGGAATTCGTAGAGGTCTCTGTACTATGTGCATTTGTCTGTGTCAGT	2033
Oy	654	GCGGTTTTCTTCTGAGAGACTCTCTATCGATGATCTTCGTAGCAATGATGTGTGT	713
Db	2032	GTTTGTGCTCTCTGGCGCAGTCTCTATTTGGATGTTGTGTGTGATGATGTGT	2091
Oy	714	GGCGATGGAATAGCTGATATATAGGACGTAAAGTTTGGTCAACTAAGATACCTTACAC	773
Db	2092	GGTATGGCTTTGTGTGACATTTGTGGAGAAAGGTATGGCTCCGGAAAGCTGCCATTCAT	2151
Oy	774	CCAAAGAAAGATTGGGAGAAAGATCCATCTTCACTCTCGGCTTCTTCATCTCCATC	833
Db	2152	GAGAACAAAGACTGGATGAGAGACATCCAAATGTTCAATTTTGGCTTCTCTTATCTGCA	2211
Oy	834	GCATTACTTATCTATTACTCAAGCCTTGGGTACCTTCAATGAACCTGGAAACGACTTG	893
Db	2212	CTGATGCTGTTCTATCTCTCTGTGCTTGGTACTTCACTGTCTGTGGATCTGGCACTT	2271

```

RESULT 11
US-10-425-114-23255
; Sequence 23255, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kowalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tadaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114

```

```

; LENGTH: 798
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: clone ID: LIB3595-006-H9_FLI
US-10-425-114-23255

Query Match          26.5%; Score 289; DB 7; Length 798;
Best Local Similarity 62.6%; Pred. No. 1.8e-74;
Matches 451; Conservative 0; Mismatches 270; Indels 0; Gaps 0;

QY      286  CAGCAGTGTGCACCAAAATTCGCTGTGTGATGATGACGTCCGAGGCCACCGTGGACAGTGTGTGCTG 345
Db       2   CGGCGGGGGGGCGCCCGCCACGCGGTGTGTGACGACGAGAGGGGTCACTGTGTATCAACCGCCG 61

QY      346  GAGCATACGGCGCTTGTCTTAAAGCTTTCAGAGCTCTCACCAGCAAAAGCTATTCAACAGA 405
Db       62  GCGCCTACTCTCTTGTGCGCGCTTTCGACGACGAGCTCACCGAGCGCGGCTCATCAAAAAG 121

QY      406  GTTTGACAGAAAGCTTGTGATATATCTTCACAGGTCTGCTTTTGTACTTGGCGGCGCA 465
Db      122  GCTTGACACGAAAGTTGTGACGTGTATCTCCGCGCTCTGTTATGATCATCTTGGCCCC 181

```


Query Match 25.6%; Score 278.8; DB 7; Length 976;
Best Local Similarity 61.6%; Pred. No. 2.2e-71;
Matches 445; Conservative 0; Mismatches 277; Indels 0; Gaps 0;

```
QY 294 GCGACGATTCGCTGTCATGACGTCGAGCACCCTGAGAGTGTGTCGAGCATAC 353
DB 204 GCGGCGTCATGCTGTCGCGGAGCGGCGGCGACGCTGCTGTCACCGCGGCGCATAC 263
QY 354 GCGCTGCTTAAGCTTGAAGTCTCACCAAGCAAGCATTCATCAAGATTGAGC 413
DB 264 TCCCTCGCGCGCTTCGAGCGCTCACCGAGCCGCCCTGCTCAACAGAGCTTGAGC 323
QY 414 AGAAGCTTGCAATATCTCTCAGGCTGCTTTCGACTTCGCTGCGCAATCTTGAC 473
DB 324 AGAAGGTTGTCATGCTATCCGAGGCTTTTTCATGCTTCAAGCCACTCTTCACG 383
QY 474 GGATCGACCGAGGCTCGATCTTGTGCTTGTTCCTTGTAGTGAATGCGTTAAGGCTT 533
DB 384 AATTCTACGATGACGCGTTCTTGCGACGCGTATGCTTCTGTAACCTGGTAAGGCTT 443
QY 534 GTTATTAACGACATTCATTTCCCAATTCGATCTTAATCAATCCGTCACAAAGAA 593
DB 444 CTCACCTACGCGGCTCGGCTTCTACTCCGACGAGCTTAGTAAATCGGTGAA 503
QY 594 GCGAGAGAGAAAGTTCCTTAAGGCTTGTTCCTAGCTTCTTCTCT 653
DB 504 GGAAGACGAGAGAAATTCGCGAGCCCTCTGTAATGTAATGCTACTGATCAAT 563
QY 654 GCGCTTTCCTCTGAGAGAGTCTCTATTCGTAATGATCTGTTAGCAATGATGTGAT 713
DB 564 GTTCTAGCTTTCGCGGAGCTCCCGCATTCGGAATCGTTCTTGATGATGAGCGGT 623
QY 714 GCGCATGGAATAGCTGATTAATGGAAGCTTAAGTTGGCTCACTAAGTACTTAAAC 773
DB 624 GGTACGCGCTTTCGACATTCGCGAGAAAGTTCGCGCTCAACCTCCATTCAC 683
QY 774 CCAAGAAAGAGTGGCGAGAAAGCATCTCCATGTTCACTTCGCTTTCATCTCCATC 833
DB 684 AAGAAAGAGCTGGCTGCGAGAGTCCGCGAGTTCATCTCGGTTCTCTCTATGCA 743
QY 834 GCATTACTTCTACTATCTCAAGCCTTGGTACTTCACTGATGAACTGGAAACGACTTG 893
DB 744 CTGATGCTGCTCTATTTCTCGGCTTGTGTTACATCAGTACAGTGGGATCAAGCGCTT 803
QY 894 CAGAGAGTGAAGATGCTCAATGCTGCGCAAGTATGAGTGCATCCATCAAGCAT 953
DB 804 GGTAAAGTGTTCGCTGCGCTGCGCAAGCTGAGTGTGATTCCTGTAACTGAT 863
QY 954 CAATTAGCGAATATTCGCTTCGCTGCTGCTACTATTTAGCTGCTTATTTAGTTTC 1013
DB 864 GTTGAGATGAATATCTGTTCTCTTGCGACCAATGTTGAGCCCTTCTGTTGTT 923
QY 1014 GG 1015
DB 924 GG 925
```

RESULT 14
US-10-425-114-26454
; Sequence 26454, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26454
; LENGTH: 937
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB4185-014-E12_FLI
US-10-425-114-26454

Query Match 25.2%; Score 275.4; DB 7; Length 937;
Best Local Similarity 62.3%; Pred. No. 2.1e-70;
Matches 449; Conservative 0; Mismatches 271; Indels 1; Gaps 1;

```
QY 286 CAGCAGTTGCGACGAATTCGCTGTCATGACGTCGAGCCACCGTGGCACTGCTGTG 345
DB 158 CGGCGCGCGCGCGCGCGCGGCTGCGAGAGCGGCGGCTACTGTCTATCAACCGCG 217
QY 346 GAGCATACGCGCTTGTAGCTTTCGAGAGTCTCACCAAGCAAGCATTCACAGCA 405
DB 218 GCGCTTACTCTCTTGTGCGGCTTTCGACGAGCTCACCGAGCGGCGCTCATCGAAAAG 277
QY 406 GTTTAGCAGAAAGCTTGTGATATCTTCAGGCTGCTTTTGTGCTTCTGCTGCGCAA 465
DB 278 GCTTGAAGAGAGAGTTGTGACGCTGCTGCGCGCTCTGTCATGTCATCTTGCGCCC 337
QY 466 TCTTACGCGATTCGACGAGGCTGATATCTTGTGCTTGTTCCTTCTGATGATGCT 525
DB 338 TGGTACGAAATTCACAGAAACAGGTAATTCGCGCGGCTGCTGCTGCTGAACTCA 397
QY 526 TAAAGCTTGTATTAACGACTATTCATTTCCCAATTCGATGCTAATCAATCCGCA 585
DB 398 TGAAGCTTCTATATATGATCTCCGCTCTACATGATGAGCTCTGTTAAATCAGTGA 457
QY 586 CAGAGAAAGGAGCAGAAAGTTCCTTAAGGCTCTTGTGCTTCTGCTTCTGCTCTTC 645
DB 458 CAGCTGAAGGAAACAGAGAAATTCGTAAGAG-CCACTATATATGCTCTGCTGCTGC 516
QY 646 TTTTCTCTGCGGTTTTCTTCTGAGAGAGTCTCTATTCGTAATGATCTCTGTTAGCA 705
DB 517 TGTTCAGGTTTATGCTCTTCTGCGGTGAGTCCCATTCGAGATGCTCTCTGTCAGTGA 576
QY 706 TGTGTGAGGATGGAATAGCTATTAATGGAAGCTTAAGTTGGGCTCACTAAGATAC 765
DB 577 TGAAGGCTGCGAGTGTTCCTCTACATTTGTTGGAAGGATATGCTCAAGCAAGCTGC 636
QY 766 CTTCACCAACCAAGAAAGTTCGAGAGAGCATCTCCATGTTCACTTCGCGCTTCTTCA 825
DB 637 CATTCATTCGGAAGAGAGTGGCGCGGAGACATCTGATGTTCACTTCTGTTCCGTC 696
QY 826 TCTTCATGCACTTACTTACTTATCTCAAGCTTGGTACTTCAATGAATGGAAG 885
DB 697 TGTCCGAGATGATGCTCTACTTCTCAAGCTTCGAGTTACATTAATGATGTTCTGGAAG 756
QY 886 GACCTTGACAGAGTGAAGATGCTCAATGCTGCGACGAGTGTGAGTGCCTACCA 945
DB 757 AGGACTTGTGATGCTGCGCTTGTGCTGACAGAGCAAGTATGAGAGCTGCTCTG 816
QY 946 TCACCGATCAATTGAGACGAATATTCGCTTCTGCTGCTACTATTTTACTGCTTAT 1005
DB 817 TGACCGAAGTTGTATGACGAATATCTGTTCTTTGGCACCATGCTGTGACTTCTTTC 876
QY 1006 T 1006
DB 877 T 877
```

RESULT 15
US-10-425-114-25671
; Sequence 25671, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong

Job time : 3420 secs

```

APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 25671
LENGTH: 723
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3957-022_E3_FLI
US-10-425-114-25671

```

Query Match	25.2%	Score 274.8	DB 7	Length 723
Best Local Similarity	63.4%	Pred No. 2.8e-70		
Matches 420, Conservative	0	Mismatches 242	Indels 0	Gaps 0

OY	345	GGAGATACGGCTGTCTTTAAGCTTGCAGAGTCTCACCAAGCGAAAGCTATTCACAG	404
Db	7	GGCGCTACTCTCTTGTGCGGCTTTCACAGAGCTCACGAGGGCGGCTATTCGAAAG	66
OY	405	AGTTTACGAGAAAGCTTGTGCATTAATCTCAGGTCTGTCTTTCTGTATTGCGTGCCCA	464
Db	67	AGCTTGACAGGAAGTTGTGCAAGTGTGCTCCGGCGTCTGTTCATGTCAATCTTGGCCC	126
OY	465	ATCTTACAGGATTCGACCGAGGCTGATACCTTGTGCTTTGTTCCGTTATGTAAGGAC	524
Db	127	CTGTTACGAATTCACAGAGCAGGATTTTTCGCGGGTTGTCCGTTCTGTAATCC	186
OY	525	TTAAGGCTGTTATTTAACGAACTATCCATTTCCCAATTGAGTCTAATCAATCCGTC	584
Db	187	ATGAGGCTTCGATATATATGACTCCGTCCTACATGATGAAGCTCTGGTAAATCAAGTG	246
OY	585	ACAAAGAAAGGAGAGCAGAAAGATTGCTTAAAGTCCCTTGTTCAGTCTTACTCTT	644
Db	247	ACAGGTGAAGAAAAACAGAGGAATTTCTGAGAGGTCCACTATTAATGCTCTGGTCTG	306
OY	645	CTTTCTCTGCGGTTTCTTCTGAGAGAGTCTCCTATCGATAGATCTCGTTACAAATG	704
Db	307	CTGTTCAAGCTTTTAGTCTTTCGGGTGATCCCATCGGATGCTCTTGTGCATG	366
OY	705	ATGTGTGTTGCGGATGAAATAGCTGATATATATGGAAGTAAATTTGGGTCACTAAGATA	764
Db	367	ATGACGGTGGGAGGTTTCGCTACAAATGTGTGAAGAGGATATGGCTCACAGGAAGCTG	426
OY	765	CCTTACAAACCAAGAAAGATTGGGCAAGGACATCTCATGTTCACTTCCGCTTCTTC	824
Db	427	CCATTCAATCGGAABAAGAGCTGGGCGGGAGACATCTGATTTCAATTCCTGGTTTCTG	486
OY	825	ATCTTCATCGCAATTACTTACTATTACTACAGCTTGGGTACCTTCAATGAATCGGAA	884
Db	487	CTGTCCGGAGATGATGCTTACTACTTCAACCTGGGTTAATTAATGATGTTATCTGGGAA	546
OY	885	ACGACCTTGACAGAGTAGCAATGATGTCAATAGTGCCACGGTGTGAGTCCGATACC	944
Db	547	GAGGCACTTGTGAAGCTGGCGCTTGTGCACTAGACGCAATTTTATTTATTTAGCTTTAT	606
OY	945	ATCACCGATCAATTAGACGACAAATATTTGCTTCTCTGGCTACTAATTTTAACTGTAT	1000
Db	607	GTGACCGAAAGTTGTAGATGACAAATATCTGTTCTTTGGCACCATGCTGGTAGCTTT	666
OY	1005	TT 1006	
Db	667	CT 668	

	Query Match	Similarity	62.3%	Score	287.4	DB	9	Length	1198	
	Best Local	Similarity	26.4%	Pred.	No. 3.3e-64					
	Matches	450	Conservative	0	Mismatches	271	Indels	0	Gaps	0
Qy	286	CAGCAGTTGCGACGAATTCGCTGTTGCATGACGTGCGAGCCACCGTGCAGTGGTTGGTG	345							
Db	372	CGCGCCCGCGCGCGCCGACAGCGGTGCTGCAGGACCGGACCGGTACATGTCATCACCCCG	433							
Qy	346	GAGCATAGCGGCTTGCTTTAAGCTTCGAGAGTCCACCAAGCGAAAGTCATTAACAGA	405							
Db	432	GCGCTACTCTCTTGTGCGCGTCTTTCGACAGAGTCCACGAGCGCGGCTCATTCGAAAGA	492							
Qy	406	GTTTGAGCAGAAAGCTTGTGCATATACCTCGAGGTCTGCTTTTCGTACTTGGTGCCAA	465							
Db	492	GCTTGAGCAGAAAGTGTGTCACGTGCATCCGCGGTCTGTGTCATGTCATCTTGGGCC	551							
Qy	466	TCTTGAGCGAATCGACCGAGGCTCGAATCTTTGCTGCTTTGTTCCGTTATGTAATGGCT	525							
Db	552	TGTTTCAGCAATTCGACAGAGCAGCGTATTTTCGCGGGTGTCCCGTCTCTAACTCCA	611							
Qy	526	TAAAGCTTTATTAACGAGCTATTCATTTCCCAATTTGATGTCATTAATTCGCTCA	585							


```

RESULT 4
US-11-096-568A-14811
; Sequence 14811, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 14811
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(1048)
; OTHER INFORMATION: Ceres Seq. ID no. 12336653
US-11-096-568A-14811

```

Query Match	Similarity	14.1%	Score 153.8	DB 9	Length 1048
Best Local	Similarity	51.9%	Pred. No. 15-25	Mismatches 342	Indels 3
Matches	372	Conservative	0		Gaps 1
Qy	304	CGCTGTCATGACGTCGGAGGCCACCGTGGCACTGCTTGTGGAGACATACGCGTTCCT	363		
Db	201	CCCTGGCCCATGACCTTAGGGCTGTGAAGTCGTACAGAGTGTGTGCGCCCTGGCTCTCA	260		
Qy	364	TAACTTGGAGAGCTCACCAAGCGAAAGTCATTCACAGAGTTTGAAGAGAACTTG	423		
Db	261	AACTCTTGGAGAGCTCGCGCAAGCCGCGGTCTTGAGAGAGAACTCAGCAGAAAGCTTG	320		
Qy	424	TGCATATCTCTCAAGTCTGCTTTCGTACTTGCGGTGGCAATCTTCAGCGAGTGAACG	483		
Db	321	TTCAATATAGCCTTGGGCTGGTATTCAGCTCTTTTGGCTCTTTTAACTCTGATGCT	380		
Qy	484	AGGCTCGATCTTTCGCTTTCGTTCGTATGATGATGGCTTAAGCTGTATTTAACG	543		
Db	381	ATATCTCTTTCCTTCTGCTGGCTAGACACAGGGGTTAACTTTAAAGATGCTTCTACGG	440		
Qy	544	GACTATCAATTTCCCAATTCGATGCTAATCAAAATCCGTCAAGAGAGAGAGACG	603		
Db	441	GGCTGGGACTTATGAAAAACAGAGCTATGTTAAATCAATGAGCCGCTCGAGATTACA	500		
Qy	604	AAAGATGCTTAAAGTCTTTCGTACGTTCTAGCTCTTCTTCTCTGGGTTTCT	663		
Db	501	GGGAATCTTCAAGGCGCCACTGTAATTAAGCTGATCAATTAATCTTTTGAAGCTCTT	560		
Qy	664	TCTGAGAGAGTCTCTATCGGTATGATCTCGTTAGCAATGATGTGGTGGCATGGA	723		
Db	561	TATGAGAACTCACCAAGTGTCTATATGACATTTATGCACTTAATGTGTGGGATGTA	620		
Qy	724	TAGCTGATATAAGGACGTAAAGTTTGGGTCAACTAAGATACCTTACACCCAGAAAGA	783		
Db	621	TAGCCGATGTTGTTGGAGAGCGCTTAGGTAAGAAAGATCTTCATATCAATCCACAAT	680		
Qy	784	GTTGGGCGAAGAGATCTTCATGTTCACTTCCTGGCTCTTCAATCTTCATGCAATTACTT	843		
Db	681	CATATGCTGGAAGCAATAGCAATGGCGGTGGCTGTTCTTGGCTCAAGTTGGATATGTC	740		
Qy	844	ACTATTACTCAAGCCTTGGGTACTTTCACATGATACGTGGAAACGACTTGACAGAGTAG	903		
Db	741	ATTACTTCAACACTTTCGTTTATATGAGAAACATGTACATGCTTT---AACTTCC	797		
Qy	904	CAATGCTCAATGTCGCCACGGTAGTGAAGTGCCTAACCCATCAATCAATTAGACG	963		
Db	798	TCTGTGTCGTGTATGCTGAGACACTCGTTGAATGCCACCCATCAGACAGAACTTGATG	857		
Qy	964	ACAAATATTCGGTCTCTCGGTACTATTTTAAAGTCTTATTTAAAGTTTGGATATT	1020		
Db	858	ACAAATTTAGCTGTTCTTTTGAATCATATCTCAATGTTGGTGAAGCTCAATCTTTGATGTT	914		

```

RESULT 5
US-10-995-561-13236
; Sequence 13236, Application US/10995561
; Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13236
LENGTH: 305312
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)_"(305312)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13236

```

```

RESULT 6
US-11-136-527-7472
; Sequence 7472, Application US/11136527
; Publication No. US2005028750A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounst, William M
; TITLE OR INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031696-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7472
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-7472

```

Best Local Similarity 56.2%; Pred. No. 1.8;
Matches 63; Conservative 6; Mismatches 43; Indels 0; Gaps 0;

Qy 22 TATCATTTTCTTATCTTATTTAGCTTGTCAAGATCTCTTCTTCTTCTTCTCTCC 81

Db 475 TCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCC 534

Qy 82 TCCCTCAAGTCTGCTTCTGTCATGCGACGACCTTACTTATCTCC 133

Db 535 TCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCC 586

RESULT 7

US-11-136-527-3376
Sequence 3376, Application US/11136527
Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION: Mounts, William M
FILE REFERENCE: 031896-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

PRIOR FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: PatentIn version 3.2

SEQ ID NO 3376

LENGTH: 2380

TYPE: DNA

ORGANISM: Rattus norvegicus

US-11-136-527-3376

Query Match 3.7%; Score 40.8; DB 12; Length 2380;
Best Local Similarity 56.2%; Pred. No. 2.2;
Matches 63; Conservative 6; Mismatches 43; Indels 0; Gaps 0;

Qy 22 TATCATTTTCTTATCTTATTTAGCTTGTCAAGATCTCTTCTTCTTCTTCTCTCC 81

Db 1455 TCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCC 1514

Qy 82 TCCCTCAAGTCTGCTTCTGTCATGCGACGACCTTACTTATCTCC 133

Db 1515 TCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCC 1566

RESULT 8

US-09-925-065A-515244/c
Sequence 515244, Application US/09925065A
Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 515244

LENGTH: 585

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-515244

Query Match 3.6%; Score 39.8; DB 6; Length 585;

Best Local Similarity 50.6%; Pred. No. 2.3;
Matches 119; Conservative 1; Mismatches 113; Indels 2; Gaps 1;

Qy 24 TCAATTTCTTATCTTATTTAGCTTGTCAAGATCTCTTCTTCTTCTTCTTCTTCTC 83

Db 389 TCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCC 330

Qy 84 CTCGAAGTCTGCTTCTGTCATGCGACGACCTTACTTCTTCTTCTTCTTCTTCTTCT 143

Db 329 CTCCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCC 272

Qy 144 CAGTTGTCGCTTCTGCGAACAATCTTGTGACGACTCAACGCTTCTTCTTCTTCTTCT 203

Db 271 CAGTTGTCGCTTCTGCGAACAATCTTGTGACGACTCAACGCTTCTTCTTCTTCTT 212

Qy 204 TTGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 258

Db 211 TTCCCTGTAGTCTCTGCAATGATGATGATGATGATGATGATGATGATGATGATG 157

RESULT 9

US-09-925-065A-655075/c
Sequence 655075, Application US/09925065A
Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 655075

LENGTH: 579

TYPE: DNA

ORGANISM: Homo sapiens

US-09-925-065A-655075

Query Match 3.6%; Score 39; DB 6; Length 579;
Best Local Similarity 52.1%; Pred. No. 3.7;
Matches 113; Conservative 0; Mismatches 100; Indels 4; Gaps 1;

Qy 79 TCTCTCTCAAGTCTGCTTCTGTCATGCGACGACCTTACTTATCTTCTGATCA 138

Db 499 TTTCTCTTCTGATCTTATATCTTACTCAATGCGAAGATGCAAGCTTACCAAGTCTCC 440

Qy 139 ATCATCAAGTGTGTGCTGTCGGAACAATCTTGTGACGACTCACCGGTTCTGTTTC---T 194

Db 439 ATATGCGAGGCTTACCTCTGTTTAAAGAAATTAACAAGTGTGATGCGCAAGGT 380

Qy 195 CTTGCTTCTTATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 254

Db 379 CATGGTGTGCTGACTCTTACGCTGCTGTTTCAATTTTCAAGCTTCTGTTCTTCTGACT 320

Qy 255 CAGTTAGTGTCTGCTTCTGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 291

Db 319 TCTACAACTGTATGATTTTCTTATCTTCTTCTGCTG 283

```

? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 45
? LENGTH: 395
? TYPE: DNA
? ORGANISM: Mycobacteria tuberculosis
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)...(395)
? OTHER INFORMATION: n = A,T,C or G
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 27, 44, 104, 119, 180, 224, 237, 245, 254, 301, 327, 370,
? LOCATION: 385, 393
? OTHER INFORMATION: n = A,T,C or G
? US-11-143-401-45

Query Match      3.5%; Score 38.2; DB 12; Length 395;
Beet Local Similarity 20.4%; Pred. NO.5.1;
Matches 48; Conservative 98; Mismatches 89; Indels 0; Gaps 0;

24 TCATTTTCCTTATCTTATGCTTTCGAATTCCTTCTTCTCTTCTCTCCCTC 83
   |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db  318 BCBIYTHCCTTCTCNCNHTTBTBKRHTSATATBCKHYCTBTBBBBIKAYCAC 259

84 CTCCAACTGAGTTCCTCCGTCGCATGCGACGAACCTTACTCTATCTCGATCAATCAT 143
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db  258 MCSNNMHTMCSBNHYHCCSSNNCDSTACCYWTTNSBBBACCTGWTYYTTBBGBMBBTB 199

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Db      198 AATCWYYSSTERTTBBCASNCYHBCQWTTTCABBBYCYTCYTTWTSBTKATBRGCGYTCWDS 139
OY      204 TTGATTTCTCTCCTCTTCTTTCATTGTTTACCGGAATGGGCTCTGTACTACT 258
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      138 CTRYTTWTBTARTSHTNCTTBTBKTRHSGDYCNKCMHWGHCBABSBHBTWST 84

RESULT 12
US-09-925-0654-512623
: Sequence 512623, Application US/09925065A
: Publication No. US20040181048A1
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single
: TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
: FILE REFERENCE: 108827,135
: CURRENT APPLICATION NUMBER: US/09/925,065A
: CURRENT FILING DATE: 2001-08-08

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? PRIOR APPLICATION NUMBER: US 60/252,147
? PRIOR FILING DATE: 2000-11-20
? PRIOR APPLICATION NUMBER: US 60/250,092
? PRIOR FILING DATE: 2000-11-30
? PRIOR APPLICATION NUMBER: US 60/261,766
? PRIOR FILING DATE: 2001-01-16
? PRIOR APPLICATION NUMBER: US 60/289,846
? PRIOR FILING DATE: 2001-05-09
? NUMBER OF SEQ ID NOS: 957086
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 512623
? LENGTH: 605
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-925-065A-512623

Query Match      3.5%; Score 37.8; DB 6; Length 605;
Best Local Similarity 52.8%; Pred. No. 7.7';
Matches 102; Conservative 1; Mismatches 88; Indels 2; Gaps 1;

Oy      56 TCTCTTTTCTTCCTTCCTTCCTCCGCAAGTCAGTTGCCCTCCGCATGGACG 115
db      315 TCCTCCTCCTCTCTTTTCTTCCTCCGCGCTCCCTCTCTTCCTCCTCCGACTCCT 374

```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2006, 19:49:20 ; Search time 24 Seconds
(without alignments)
1218.746 Million cell updates/sec

Title: US-10-634-548-2
Perfect score: 1536
Sequence: 1 MAATLPLSPINHQLCRFGNN.....DDNISVPLATILAAVLSFGY 304

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum March 0%
Maximum March 100%
Listing first 45 summaries

Database :
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1536	100.0	304	2 T48445	hypothetical prote
2	195	12.7	233	2 S76857	hypothetical prote
3	191	12.4	190	2 G70433	hypothetical prote
4	184.5	12.0	211	2 D69413	conserved hypotet
5	167.5	10.9	246	2 A69013	conserved hypotet
6	164.5	10.7	179	2 AD2007	hypothetical prote
7	153.5	10.0	290	2 S58323	probable membrane
8	149	9.7	215	2 T45229	probable F420H2-de
9	144.5	9.4	519	2 JQ0124	membrane protein S
10	143.5	9.3	203	2 H75102	hypothetical prote
11	142.5	9.3	202	2 C71084	hypothetical prote
12	139.5	9.1	204	2 D71648	hypothetical prote
13	131.5	8.6	204	2 C97866	hypothetical prote
14	126	8.0	465	2 T41511	probable dolichol
15	123	8.0	215	2 H90141	conserved hypotet
16	119	7.7	257	2 C71265	hypothetical prote
17	114.5	7.5	191	2 H64441	hypothetical prote
18	113.5	7.4	207	2 D70151	conserved hypotet
19	112	7.3	456	2 H96902	membrane protein,
20	109	7.1	396	2 F69813	multidrug-efflux t
21	105.5	6.9	218	2 T40365	conserved hypotet
22	104.5	6.8	183	2 F69049	conserved hypotet
23	104.5	6.8	653	2 C82580	oligopeptide trans
24	104	6.8	598	2 T48980	hypothetical prote
25	103	6.7	545	2 S59143	MADH2 dehydrogenas
26	102.5	6.6	405	2 AC1193	hypothetical prote
27	102	6.6	654	2 T14202	MADH2 dehydrogenas
28	100.5	6.5	432	2 F83903	hypothetical prote
29	100.5	6.5	527	2 T03427	hypothetical prote

30	100.5	6.5	550	2 AF3244	conserved hypotet
31	100	6.5	521	2 S74569	MADH2 dehydrogenas
32	99.5	6.5	309	2 A82944	ribose/galactose A
33	99.5	6.5	373	2 AB1223	ethanolamine-utili
34	98	6.4	328	2 H84061	ferriochrome ABC tr
35	98	6.4	404	2 AF0034	probable integral
36	97.5	6.3	290	2 T06856	hypothetical prote
37	97.5	6.3	500	2 H95276	probable transmemb
38	97	6.3	430	2 P70016	purine permease ho
39	97	6.3	430	2 C97160	uracil permease ur
40	97	6.3	551	2 D71969	l-lactate permease
41	96.5	6.3	633	2 S82153	PTS system, fructo
42	95.5	6.2	288	2 G64102	phosphatidate cyti
43	95.5	6.2	373	2 AB1576	E. coli ethanolami
44	95.5	6.2	460	2 A39938	phosphotransferase
45	95.5	6.2	551	2 B64537	l-lactate permease

ALIGNMENTS

RESULT 1
T48445
hypothetical protein T32M21.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T48445
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysbaert, C.; Daseville, R.; De Clerck, R.; De
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 2000
A:Reference number: 224487
A:Accession: T48445
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-304 <BEV>
A:Cross-references: UNIPROT:Q9LZ76; UNIPARC:UPI00000A81C7; EMBL:AL162875
A:Experimental source: cultivar Columbia; BAC clone T32M21
C:Genetics:
A:Map position: 5
A:introns: 99/3; 122/2; 166/2; 205/1; 243/2
A:Note: T32M21.90

Query Match 100.0%; Score 1536; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 3.5e-119;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAATLPLSPINHQLCRFGNNSLTTHRCSPGFLISSPCFTGLTGMGATQLRARRSLISS 60
Db 1 MAATLPLSPINHQLCRFGNNSLTTHRCSPGFLISSPCFTGLTGMGATQLRARRSLISS 60

Qy 61 AATNSLHDVGATVAVTGGAYALVSPESITKRNVIQOISRLCVITLSGLLVLAWPI 120
Db 61 AATNSLHDVGATVAVTGGAYALVSPESITKRNVIQOISRLCVITLSGLLVLAWPI 120

Qy 121 FSGSTEARYPFAFPLVNLGLRLVINGLSISPSNLSISVTRREGRAEELKGPLFYVALT 180
Db 121 FSGSTEARYPFAFPLVNLGLRLVINGLSISPSNLSISVTRREGRAEELKGPLFYVALT 180

Qy 181 FSAVFFWRRESPIGMSLMMCGGDIADIMGKRGSKTIPNPRKSNAGSISMEIFGFFI 240
Db 181 FSAVFFWRRESPIGMSLMMCGGDIADIMGKRGSKTIPNPRKSNAGSISMEIFGFFI 240

Qy 241 SIALITYYSSIGYLAHNMETTLQRVANVSVATVYESLPITDQDDNISVPLATILAAVL 300
Db 241 SIALITYYSSIGYLAHNMETTLQRVANVSVATVYESLPITDQDDNISVPLATILAAVL 300

Qy 301 SFGY 304
Db 301 SFGY 304

RESULT 2
S76857

hypothetical protein - *Synechocystis* sp. (strain PCC 6803)

C:Species: *Synechocystis* sp.

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S76857

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimizu, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yaeuda DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76857

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-233 <KAN>

A:Cross-references: UNIPROT:P74653; UNIPARC:UPI00000C093C; EMBL:D90917; GB:AB001339; NID A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 12.7%; Score 195; DB 2; Length 233;

Best Local Similarity 29.1%; Pred. No. 8.4e-09;

Matches 69; Conservative 49; Mismatches 83; Indels 36; Gaps 12;

QY 71 VGATVAVGAVYALVLSFESLTKNVIOQSRLVHLISGLFVLA----PIFGSGTE 126

DB 17 VGLATVYIG---AVLTALRLNLRLSLPAEYTRKIVHIGAGVVLIAWMLSI PGWVGAI - 72

QY 127 ARYPAFPLVNGRLVNGLSISPNMLKSVTRGAEELKGPLFYVAL-LFSAVF 185

DB 73 AGVFPA-----GIVLSIRLPILPS---LESVGHS-----YTLVYALISGLVGGF 117

QY 186 FWRSEPI-GMISLAWCGGDIADIMGRKFGSTKIP-YNPRKWSAGISMPFGFISIA 243

DB 118 FSLGPIPAFALIGLVMAAGDGLAALVGGRGHRQVGFGRKSWEGTLTAVLASLVTVV 177

QY 244 LLYYSSISGLYHNMWETTLQRYAVMSVATVVESEPTDQD-DNISVPLATILAAV 299

DB 178 FLSY--TEGFG-----TVIVLVAVGTVAIASAGLESFGRMGIDMLTVPLGSALIAW 225

QY 244 LLYYSSISGLYHNMWETTLQRYAVMSVATVVESEPTDQD-DNISVPLATILAAV 299

DB 178 FLSY--TEGFG-----TVIVLVAVGTVAIASAGLESFGRMGIDMLTVPLGSALIAW 225

QY 244 LLYYSSISGLYHNMWETTLQRYAVMSVATVVESEPTDQD-DNISVPLATILAAV 299

DB 178 FLSY--TEGFG-----TVIVLVAVGTVAIASAGLESFGRMGIDMLTVPLGSALIAW 225

QY 244 LLYYSSISGLYHNMWETTLQRYAVMSVATVVESEPTDQD-DNISVPLATILAAV 299

DB 178 FLSY--TEGFG-----TVIVLVAVGTVAIASAGLESFGRMGIDMLTVPLGSALIAW 225

QY 244 LLYYSSISGLYHNMWETTLQRYAVMSVATVVESEPTDQD-DNISVPLATILAAV 299

DB 178 FLSY--TEGFG-----TVIVLVAVGTVAIASAGLESFGRMGIDMLTVPLGSALIAW 225

QY 244 LLYYSSISGLYHNMWETTLQRYAVMSVATVVESEPTDQD-DNISVPLATILAAV 299

DB 178 FLSY--TEGFG-----TVIVLVAVGTVAIASAGLESFGRMGIDMLTVPLGSALIAW 225

QY 244 LLYYSSISGLYHNMWETTLQRYAVMSVATVVESEPTDQD-DNISVPLATILAAV 299

DB 178 FLSY--TEGFG-----TVIVLVAVGTVAIASAGLESFGRMGIDMLTVPLGSALIAW 225

QY 244 LLYYSSISGLYHNMWETTLQRYAVMSVATVVESEPTDQD-DNISVPLATILAAV 299

DB 178 FLSY--TEGFG-----TVIVLVAVGTVAIASAGLESFGRMGIDMLTVPLGSALIAW 225

QY 244 LLYYSSISGLYHNMWETTLQRYAVMSVATVVESEPTDQD-DNISVPLATILAAV 299

DB 178 FLSY--TEGFG-----TVIVLVAVGTVAIASAGLESFGRMGIDMLTVPLGSALIAW 225

QY 244 LLYYSSISGLYHNMWETTLQRYAVMSVATVVESEPTDQD-DNISVPLATILAAV 299

DB 178 FLSY--TEGFG-----TVIVLVAVGTVAIASAGLESFGRMGIDMLTVPLGSALIAW 225

QY 244 LLYYSSISGLYHNMWETTLQRYAVMSVATVVESEPTDQD-DNISVPLATILAAV 299

DB 178 FLSY--TEGFG-----TVIVLVAVGTVAIASAGLESFGRMGIDMLTVPLGSALIAW 225

QY 244 LLYYSSISGLYHNMWETTLQRYAVMSVATVVESEPTDQD-DNISVPLATILAAV 299

DB 178 FLSY--TEGFG-----TVIVLVAVGTVAIASAGLESFGRMGIDMLTVPLGSALIAW 225

QY 244 LLYYSSISGLYHNMWETTLQRYAVMSVATVVESEPTDQD-DNISVPLATILAAV 299

DB 178 FLSY--TEGFG-----TVIVLVAVGTVAIASAGLESFGRMGIDMLTVPLGSALIAW 225

QY 244 LLYYSSISGLYHNMWETTLQRYAVMSVATVVESEPTDQD-DNISVPLATILAAV 299

DB 178 FLSY--TEGFG-----TVIVLVAVGTVAIASAGLESFGRMGIDMLTVPLGSALIAW 225

QY 244 LLYYSSISGLYHNMWETTLQRYAVMSVATVVESEPTDQD-DNISVPLATILAAV 299

DB 178 FLSY--TEGFG-----TVIVLVAVGTVAIASAGLESFGRMGIDMLTVPLGSALIAW 225

DB 112 FSLGVYFGRRLKFLYNPKSLBECTLAFTASF---IGLLLF-----TDFCEA 156

QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

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QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

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DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

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QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

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DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

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DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

DB 112 FSLGVYFGRRLKFLYNPKSLBECTLAFTASF---IGLLLF-----TDFCEA 156

QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186

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QY 266 AMVSMVATVVESEPTDQD-DNISVPLATILAAV 300

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DB 157 FVLSICAVLESPL--KDDNFIIP---VLASLT 186


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QY 75 VAVGGAVYALVYFSESLTKRANVYIQOGLSHKVIHLSG--LLPLVAMPISGSGTEARYPAAF 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 43 VAVL-----LVBERFLGDR-----PVLKKFPHIHWGNIPLTL--PLFESNLVTTFPLAA-- 90
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 134 VPLVNGRLRVINGLSISPNSMILKSVYTBREAGAEELDKPLFVYVALLFSAVFWRBSPIG 193
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 91 APFI-----LITFL--LSPYSPLRVKHRASVYGHG--GLVYYSISWTLIAYLFEADWIT 142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 194 MISLAWMGCGDGIADIMGRKFGSTKLP--YNPKKSAGSISMPITGFPISTALLYYTSSLG 252
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 143 GIGIAAMSXYDGDPASLTGERFGRTFFSVLGDCKSLGEGSIQMFIIILLVNLPVLLYYYSQ--G 201
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 253 YLHMNMTTLQRVAVMSVATVYESLPITDQDDNIVSPLATITLAAVLSFG 303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 202 F-----TPYILISVALSVTEUHL--TPRGIDNLTQFCGAV--AAIYILG 242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 6

hypothetical protein all1610 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Name: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AD2007
R:Kaneko, T., Nakamura, Y., Wolk, C.P., Kuriitz, T., Saeamato, S., Matanabe, A., Iriguchi,
N., Nakazaki, N., Shimizu, S., Sugimoto, M., Takazawa, M., Yamada, M., Tabata, S.
DNA Rep. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AD2007
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-179 <KUR>
A:Cross-references: UNIPROT:Q8YWK3, UNIPARC:UPI00000CEI49; GB:BA000019; PIDD:BA877976.1
A:Experimental source: strain PCC 7120
C:Genetics:
C:Gene: all1610

	Query Match	10.7%	Score 164.5	DB 2	Length 179
	Best Local Similarity	27.5%	Pred. No. 26-06		
	Matches	53	Conservative	40	Mismatches 71, Indels 29, Gaps 8
Qy	113	LFLVLTAMPI--FGSGTEARYEPAFVPLVNGELRVINGISISPNSMLINSVTREGRAEBLL	169		
	:	:::	:	:::	:
	:	:::	:	:::	:
Db	1	MILATMWIDIPASVIGASVVASITLTLSTYIFPLLPG-----INNVGRQS-----	45		
Qy	170	KGPLFYVALLEPSANFEW--RESPIGWTSLAWCGDGDGIADIMGRKRFSGTRP-R-INPKRS	226		
	:	:::	:	:::	:
	:	:::	:	:::	:
Db	46	LGTFFFAASVGILLVAFMHIOOPYAAGMMVMANGDGIALAVGGRGFGHKKYLGAQGS	105		
Qy	227	WAGSIMEIFGFHFISIALLYSSLSGYIHMNETTLQRVAMYSMAVAVESLPITDOLD	286		
	:	:::	:	:::	:
	:	:::	:	:::	:
Db	106	MEGSTMTALASYLVCSLL-----LGVLGNAVQTWLVSIA-VAPATSLSEAFSLGCV--D	157		
Qy	287	NISVPLATILAAY	299		
	:	:::	:	:::	:
	:	:::	:	:::	:
Db	158	NUTVPLGSAATAAF	170		

RESULT 7

probable membrane protein YOR11C - yeast (*Saccharomyces cerevisiae*)
N/Alternate names: hypothetical protein O6111
C/Species: *Saccharomyces cerevisiae*
C/Date: 13-Jan-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004
A/Accession: S58523, S57217, S71591
R/Pearson, B.M.; Hernandez, Y.; Wolf, S.S.; Kalogeropoulos, A.; Schweizer, M.
submitted to the EMBL data library, August 1995
A/Reference number: S58318
A/Accession: S58523
A/Molecule type: DNA
A/Residues: 1-290 <PEA>

A; Cross-references: UNIPROT:Q12382; UNIPARC:UPI0000065B14; EMBL:X90565; NID:G940836; PDB:1A96
R; Pearson, B.M.; Hernando, Y.; Kalogeropoulos, A.; Schweizer, M.
submitted to the Protein Sequence Database, July 1996
A; Reference number: S67213

Query Match	10.0%;	Score 153.5;	DB 2;	Length 290;
Best Local Similarity	26.3%;	Pred. No. 2.9e-05;		
Matches	61;	Conservative 42;	Mismatches 78;	Indels 51;
				Gaps 10

```

QY      80 GAVALLVTFEELTEKKNVQOQSLSRLLVHILSGLEVLVAMPFFSGSTEARYPAAFPVLNG 130
QY      84 GFITLLYLTQGINKNVLMPLIYAFILFIDLI  RLMMPPF----- 124
DB
QY      140 LRLVINGLSISPNMILKSVTREGRAEEL-LKGEPLFYVALILBSAVFPWFRESPIGIMSL 197
DB      125 -----NMLYCRTGVALMKRKKHHYTVNGVLMILGLIFESFNFFSKD-VTLISL 170
QY      198 AMMGCGDGLADIMGRKFG-STKLPYNRKXSMAGISNFIQGFISIALLYYSSLSGLYH 255
DB      171 FILMSDTPAAATIGKRYCHLTPKAAARN-KSLAGSIAAFYVG-VITCWPFYGYFVPAVS 227
QY      256 MN-----W-ETTLQRYAAMSVAATVESLPITQDL---DDNISVPLATIL 296
DB      228 VNKGEIGIOWSEITSLNMLSLILGAGVAAALSEGIDILRNMDNFTIIPVALSL 279

```

RESULT

T45229
probable F420H2-dehydrogenase [imported] - Methanoblobus tindarius
M.Alternate names: ffdD protein
C.Species: Methanoblobus tindarius
C.Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C.Accession: T45229
R.Wertheberg, D.U.; Branne, A.; Ruppert, C.; Mueller, V.; Herzberg, C.; Gottschalk, G.;
submitted to: The EMBL Data Library, September 1998
A.Description: The F420H2-dehydrogenase from Methanoblobus tindarius: Cloning of the ffd
A.Reference number: Z22947
A.Accession: T45229
A.Status: Preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-215 <WISS>
A.Cross-references: UNIPROT:Q9UXN7; UNIPARC:UP100000624B8; EMBL:A011519; PDB: CAB56642
A.Experimental source: DSM 2278
A.Genetic(s)
A.Gene: ffdD

Query Match	9.7%;	Score 149;	DB 2;	Length 215;
Best Local Similarity	24.3%;	Pred. No. 4.7e-05;		
Matches	53;	Conservative	45;	Mismatches 66;
		Indels	54;	Gaps 10

```

Oy      103 KRLVHILSLGLFVLAAMPFSGSTEARYPAAVPLVNGRLVNLGSLSPNSMLTKS----- 158
Db      17  RKLHVHISGLAVI---PLVYFFETSLVLF-----LEVF-PIVSLAFLRKAYOP 67
Oy      159 -----VTRGRAAE---LTKGELFYVLAALFSAVFWBESPIGMI--SLAMMCGGDGIADI 209
Db      68  VCDMIRNRGRKKENYLPKATULLINTGILISYFLF-----PNVYCAIMATIALGDGIATV 123
Oy      210 MGRKFGSTKIPYNNPKRSNAGSISMFIFGF-----FISIALITYSSLGILHM 256
Db      124 AGEFFGKKNLPYSEKRTYEGTMAGIIAFASTVIFVSPVQALFSGVGLFIESYIG---- 179
Oy      257 MWETTLQAVAMVSMVATVESLPITDQLDNDISPIAFL 294
Db      180 ---RDLRTGSSINSFNLTK-----NDNLVPLIAS 206

RESULT 9
J00124
membrane protein SEC59 - yeast (Saccharomyces cerevisiae)
N|Alternate names: protein YMR270.17c; protein YMR013c
C|Species: Saccharomyces cerevisiae
C|Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
A|Accession: J00124; S53044
R|Bernstein, M.; Kepes, F.; Schekman, R.
Mol. Cell. Biol. 9, 1191-1199, 1989
A|Title: SEC59 encodes a membrane protein required for core glycosylation in Saccharomyces
A|Reference number: J00124; MUID:89261723; PMID:2657387
A|Accession: J00124
A|Molecule type: DNA
A|Residues: 1-519 <BER>
A|Cross-references: UNIPROT:P20048; UNIPARC:UPI00001355EA; EMBL:M25779; NID:g172567; PIR
R|Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, March 1995
A|Reference number: S53048
A|Accession: S53044
A|Molecule type: DNA
A|Residues: 1-519 <DEV>
A|Cross-references: UNIPARC:UPI00001355EA, EMBL:Z46613; NID:g728645; PID:g728662; MIPS:X
A|Experimental source: strain AB972
C|Comment: This protein acts either directly or indirectly in the biosynthesis of dolich
C|Genetics:
A|Gene: SGD:SEC59
A|Cross-references: SGD:S0004615; MIPS:YMR013c
A|Map position: 13R
C|Keywords: glycoprotein; transmembrane protein
F|87-103/Domain: transmembrane #status predicted <TM1>
F|158-174/Domain: transmembrane #status predicted <TM2>
F|181-197/Domain: transmembrane #status predicted <TM3>
F|229-245/Domain: transmembrane #status predicted <TM4>
F|260-276/Domain: transmembrane #status predicted <TM5>
F|301-317/Domain: transmembrane #status predicted <TM6>
F|397-413/Domain: transmembrane #status predicted <TM7>
F|452-466/Domain: transmembrane #status predicted <TM8>
F|503-519/Domain: transmembrane #status predicted <TM9>
F|326/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match          9.4%; Score 144.5; DB 2; Length 519;
Best Local Similarity 25.3%; Pred. No. 0.00031;
Matches 57; Conservative 51; Mismatches 74; Indels 43; Gaps 12;

Oy      64  IVLSPES-ITKKNVQQSISRLVHILSGLFVLAAMPFSGSTEARYPAAVPLVNGRL 142
Db      309  LTLSPISLIEKDSISLNTSRKLMHF---ITFLIIPFQDS-----NEVXI 353
Oy      143  VING---LSISPSMLIKSVTRGRAEEL-----KGPLFY-VIALLF--SAVFF 186
Db      354  ALSGITPVPLSLIEYIRFQNLPLGSAIELQLRRPADRDHSGPLISVYLILFGISTPL 413
Oy      187  WESPIGIMSLAMCGGDGIADIMGRKFGSTKIPYNNPKRSNAGSISMFIFGFISIAL 246
Db      414  MNNSPMGLIGLGI---GSLASIIKRYGRIRFMK-GTQKTEGLTAFTVTSFIVCLVLR 469

```

[illegible]

Db 1 MSLKELERKALHMTGLSVPLIYALGKSAITPVLIIFI-----FLALBPRLGE 52
 Qy 139 GLRLVINGLSISPNML-----IKSVTRREGAEELKGPLFYVALLPFAVFPRESPI 192
 Db 53 GLRLVNEKGLPIPEEVTEKIEREIDGIARE-REKGIAMHYFTIALLLVLYLFPREVAI 111
 Qy 193 GMISLMMCGDGIADIMGRKFGSTKIPYNPBKSWAGSISMFIQGFISIALLYYSSLSG 252
 Db 112 GSISVATL--GDMAAIIIGKSGRHR--FKNGKSVESGLAFITGLLITLTPV----- 160
 Qy 253 YLHNMETTLQORVANVSVATVVE--SLPTDQLDNDISVPLATILAAVLS 301
 Db 161 -----GLKMAALLASLVGMIVVEFYGLP-----PDDNFSNOALAIATITLYLA 199

RESULT 12

hypothetical protein RP860 - Rickettsia prowazekii
 N:Alternate names: hypothetical protein dnag 5'-region
 C:Species: Rickettsia prowazekii
 C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
 C:Accession: D11648; A46754
 R:Anderson, S.G.E.; ZomorodiPour, A.; Anderson, J.O.; Slicheritz-Ponten, T.; Alenmark, U
 Nature 396, 133-140, 1998
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
 A:Reference number: A71630; MUID:99039499; PMID:9823893
 A:Accession: D11648
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-204 <AND>
 A:Cross-references: UNIPROT:P41078; UNIPARC:UPI0000139D6E; GB:AJ235273; GB:AJ235269; NID
 A:Experimental source: strain Madrid E
 R:Mark, G.L.; Wood, D.O.
 Gene 123, 121-125, 1993
 A:Title: Characterization of the gene coding for the Rickettsia prowazekii DNA primase
 A:Reference number: J05394; MUID:93138420; PMID:8422995
 A:Accession: A46754
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 177-204 <MAR>
 A:Cross-references: UNIPARC:UPI000017AB2C
 C:Genetics:
 A:Gene: RP860

Query Match 9.1%; Score 139.5; DB 2; Length 204;
 Best Local Similarity 26.9%; Pred. No. 0.00027;
 Matches 59; Conservative 41; Mismatches 74; Indels 45; Gaps 11;
 Qy 103 RKLVIHISGLLPVLAAMPFPGSGTEARYPFAVFP--LVNGLRLVINGLSI-----SPNSM 154
 Db 12 RKIFH-LSAIFPM-----FYLFVPRIALALFLPITSITLYLDVIRHNNAK 57
 Qy 155 LIKSVTR-----EGRAEELKGPLFYVALLPFAVFPWRESPIGMTSLAMCGD 205
 Db 58 IRKVTTFPFSKIRLKENNGTFALSGISFMMLGFFLSILPKN--LVICSMILITISDC 115
 Qy 206 IADIMGRKFGSTKIPYNPBKSWAGSISMFIQGFISIALLYYSSLSGLYHNMETTLQORV 265
 Db 116 LAAVLGKIGNS---LNGKSIAGSTFPFSALPISI-LVYFY--LGY-----NTSPFI 164
 Qy 266 AMVSMVATVVESSLPTDQLDNDISVPLATILAAVLSFGY 304
 Db 165 IISCIQATVAFYPSKIRINDNISIPLSYCLSTTI-FPY 202

RESULT 13

C97866
 hypothetical protein RC1331 [imported] - Rickettsia conorii (strain Malish 7)
 C:Species: Rickettsia conorii
 C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C:Accession: C97866
 R:Ogata, H.; Audic, S.; Reneato-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rd
 Science 293, 2093-2098, 2001

A:Title: Mechanisms of evolution in Rickettsia conorii and Rickettsia prowazekii.
 A:Reference number: A97700; MUID:21442074; PMID:11557893
 A:Accession: C97866
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-204 <KUR>
 A:Cross-references: UNIPROT:Q92PZ6; UNIPARC:UPI00000CC08B; GB:AE006914; PIDN:AAI03869.1;
 C:Genetics:
 A:Gene: RC1331

Query Match 8.6%; Score 131.5; DB 2; Length 204;
 Best Local Similarity 26.0%; Pred. No. 0.0012;
 Matches 57; Conservative 43; Mismatches 72; Indels 47; Gaps 11;

Qy 103 RKLVIHISGLLPVLAAMPFPGSGTEARYPFAVFP-----LVNGLRLVINGLSISPN 153
 Db 12 RKIFH-LSAIFPLY-----LFIPRTAMTLFIITATLYLD-VSRHNN 56
 Qy 154 MLISVTR-----EGRAEELKGPLFYVALLPFAVFPWRESPIGMTSLAMCGD 204
 Db 57 TISFVTRFSPKVRLEENNGSFALSGVSEFMWIGFFLTALPKN--LVICSMILITISD 114
 Qy 205 GIADIMGRKFGSTKIPYNPBKSWAGSISMFIQGFISIALLYYSSLSGLYHNMETTLQOR 264
 Db 115 CLAAVLGKIGNS---LNGKSIAGSTFPFSALPISI-LVYFY--LGY-----NTSPFI 163
 Qy 265 AMVSMVATVVESSLPTDQLDNDISVPLATILAAVLSF 302
 Db 164 IISCIQATVAFYPSKIRINDNISIPLSYCLSTALISY 202

RESULT 14

T41511
 Probable dolichol kinase - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T41511
 R:Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, March 1999
 A:Reference number: Z21999
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Accession: T41511
 A:Molecule type: DNA
 A:Residues: 1-465 <MR>
 A:Cross-references: UNIPROT:Q9Y7T6; UNIPARC:UPI0000069554; EMBL:AL049522; PIDN:CAE40014.
 A:Experimental source: strain 972h-; cosmid c63
 C:Genetics:
 A:Gene: SPDB:SPDC63.10C
 A:Map position: 3
 A:Introns: 77/2; 106/3; 118/2

Query Match 8.2%; Score 126; DB 2; Length 465;
 Best Local Similarity 19.9%; Pred. No. 0.0092;
 Matches 79; Conservative 51; Mismatches 112; Indels 154; Gaps 19;

Qy 17 FGNNSLTTR-----PCSGEPLISSPCF--GLTNGSGATQPARSLISSAVAT 64
 Db 94 FGNSVLYHMYTWMALYCFRWGTFPIEGILCTGLTGLCPAT----- 138
 Qy 65 NSLHDVGAIVAVLGAVALVSPESLTGNVIGQSLSRK-----LVHISGLLF 114
 Db 139 --PSYEVSPVSVLSG--VLISLPTILANCLIKLAALHLSALPTTCLITFYPSALLV 194
 Qy 115 VL--AV-----PIFS-----GSTE 126
 Db 195 FLVRSRVVAGQLQAPVWLFNQIFSHRNSLTRIKIIMWIIICGCFPIILSNRNNPL 254
 Qy 127 ARYFAA-----FYPL-----VNGRLVING 146
 Db 255 GKYPTEDEVINFRKRYHALVVFLEPVCCLDPHFLHSFGVLFIFLVEGRI--- 310
 Qy 147 LSIISPNMLIKSVTRREGAEELKGPLF--YVALLPFAVFPW---RESPIGMISL--A 198

Db 311 LRKLPFGKMIHEPLMEYTDNRDHRKGLPISHTYLLIGCAIPWTSMNAKGVPAVELLVG 370

Qy 199 MMC--GGSDGADIIMGRKPGSTKIPYPRKSWAGSIMFIFGEPFISIALTYSSGLYIM 256

Db 371 VLCLGCGDSMAISIIGRFGKRRIS-KTINSISG-----VFASISVFLVHLTLQA--FHV 422

Qy 257 NMETTLQRYAMVSMATVVSLEPIYQDDNDSIVPL 292

Db 423 CPSTVFETKTLFMSLCTALIEGVSTE--NDNLLTP 455

RESULT 15

conserved hypotheical protein [imported] - Sulfolobus solfataricus
C|Species: Sulfolobus solfataricus
C|Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C|Accession: H90141
R|She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.U.; Chan
Jong, I.; Jeffries, A.C.; Kozera, C.W.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A|Description: Sulfolobus solfataricus complete genome.
A|Reference number: A99139
A|Accession: H90141
A|Status: preliminary
A|Molecule type: DNA
A|Residues: 1-215 <KUB>
A|Cross-references: UNIPROT:Q981C1; UNIPARC:UPI0000064170; GB:AE006641; NID:g13813155; E
C|GenBank:
A|Gene: SS00024
C|Superfamily: Aeropyrum pernix hypotheical protein ABE2054

Query Match	8.0%	Score 123	DB 2	length 215
Best Local Similarity	25.4%	Pred. No. 0.0066		
Matches	54	Conservative	41	Mismatches 66; Indels 52; Gaps 12
Qy	101	LSRKLVHIL-SGLFLVLA	WPFGSGTEARFAA	VPVLYNGELVINGISISNSMLIKSV 159
Db	37	YTRKAIHMLGGIVAVL	SPFVEN-----SPLVILITSY	ILIMVYLTI--RVLRKEM 85
Qy	160	TREGAAELKQPLRVY	VALLPFAVP-----FWRESF---	IGMISLAWGCGDGA 207
Db	86	SWEMDKENI--GEVFF--	AFSGVYLLVMFI	LDPENYNWSTIDLIVAVLPLIMSGDGI 141
Qy	208	DIMGRKFGSTKLI	PNYPRKSWAGSIS	IMFIFGPEISIALLYVSSLCYLHNMWETTLQRYAM 267
Db	142	GIL-RNF-----	VYKR-----VKGLMSGM	MLFCATGVGFVNLIGLI----- 180
Qy	268	VSMVATVYESLPIT	QDLQDNI	ISVPLATILAAVL 300
Db	181	AGILATVALLP---	YIDNISVPLFSL	FVLVL 210

Search completed: March 16, 2006, 19:51:29
Job time : 27 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 BioCeleration Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2006, 19:47:55 ; Search time 110 Seconds

(without alignments)
1949.824 Million cell updates/sec

Title: US-10-634-548-2
Perfect score: 1536
Sequence: 1 MAATLPSPIHQCRGNM.....DDNISVPLATLAAVLSFGY 304

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1536	100.0	304	09L276_ARATH	09L276 arabidopsis
2	1531	99.7	304	084WC0_ARATH	084WC0 arabidopsis
3	1523	99.2	304	08LF61_ARATH	08LF61 arabidopsis
4	791.5	51.5	314	07XR51_ORYSA	07XR51 oryza sativ
5	565.5	36.8	246	05N9J9_ORYSA	05N9J9 oryza sativ
6	531.5	34.6	307	067ZM7_ARATH	067ZM7 arabidopsis
7	530.5	34.5	307	067ZM1_ARATH	067ZM1 arabidopsis
8	526.5	34.3	307	08LAW9_ARATH	08LAW9 arabidopsis
9	455.5	29.7	517	09LV00_ARATH	09LV00 arabidopsis
10	309.5	20.1	1144	086HKE_DICDI	086HKE dictyosteli
11	285	18.6	228	05SA10_DICDI	05SA10 dictyosteli
12	257	16.7	223	050PDE_ENTHI	050PDE entamoeba h
13	245.5	16.0	230	050VQ1_ENTHI	050VQ1 entamoeba h
14	234	15.2	237	08KB08_CHLITE	08KB08 chlorobium
15	230	15.0	230	050LW4_ENTHI	050LW4 entamoeba h
16	195	12.7	233	P74653_SYNY3	P74653 synecocyst
17	191	12.4	190	067497_AQUAE	067497 aquifex aeo
18	184.5	12.0	211	028960_ARCFU	028960 archaeoglob
19	180	11.7	312	06KZ85_PICTO	06KZ85 picophyllus
20	173	11.3	317	075313_ASHGO	075313 ashbya goss
21	167.5	10.9	246	027171_METTH	027171 methanobact
22	164.5	10.7	179	08YWK3_ANASP	08YWK3 anabaena sp
23	163	10.6	315	0978U8_THEVO	0978U8 thermoplasma
24	161	10.5	217	07V9G9_PROMA	07V9G9 prochlorococ
25	159	10.4	283	06CKR7_KLUJA	06CKR7 kluyveromyc
26	158	10.3	208	073J58_TREDE	073J58 treponema d
27	157	10.2	214	08DHCO_STYEL	08DHCO synechococc
28	156.5	10.2	217	05N4S4_SYNP6	05N4S4 synechococc
29	156	10.2	217	07V3U3_PROMM	07V3U3 prochlorococ
30	153.5	10.0	290	012382_YEAST	012382 saccharomyc
31	149	9.7	215	09UXN7_METTI	09UXN7 methanobabu

32	146	9.5	216	2	07UD5_SYNPK	07UD5 synechococc
33	145.5	9.5	193	2	08TMQ4_METXA	08TMQ4 methanopyru
34	144.5	9.4	519	1	SEC53_YEAST	P20048 saccharomyc
35	143.5	9.3	203	2	09UZD4_PRRAB	09UZD4 pyrococcus
36	143	9.3	223	2	08Q0A6_METWA	08Q0A6 methanosarc
37	142.5	9.3	202	2	058680_PRRHO	058680 pyrococcus
38	142.5	9.3	227	2	07NGM2_GLOVI	07NGM2 gloeobacter
39	140	9.1	281	2	06FO20_CANCA	06FO20 candida gla
40	139.5	9.1	204	1	Y860_RICPR	P41078 rickettsia
41	139.5	9.1	384	2	Q5YIM5_CRYNE	Q5YIM5 cryococcu
42	136	8.9	225	2	08TPA4_METNA	08TPA4 methanosarc
43	135	8.8	204	2	06BVQ3_RICTY	06BVQ3 rickettsia
44	134	8.7	282	2	09HLC3_THIAC	09HLC3 thermoplasma
45	132.5	8.6	216	2	Q4JC44_SULAC	Q4JC44 sulfolobus

09L276_ARATH	PRELIMINARY;	PRT;	304 AA.
09L276;			
DT 01-OCT-2000 (TREMBLrel. 15, Created)			
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)			
DE Hypothetical protein 132M21_90 (A55904450).			
GN Name=132M21_90;			
OS Arabidopsis thaliana (Mouse-ear cress).			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.			
OX NCBI_TaxID=3702;			
LN [1]			
RP NUCLEOTIDE SEQUENCE.			
RA Bevan M., Terryn N., Ardiles W., Buysbaert C., Dasseville R.,			
RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,			
RA Villarroel R., Gielens J., Van Montagu M., Bancroft I., Mewes H.W.,			
RA Rudd S., Lemcke K., Mayer K.F.X.;			
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN [2]			
RP NUCLEOTIDE SEQUENCE.			
RA EU Arabidopsis sequencing project;			
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN [3]			
RP NUCLEOTIDE SEQUENCE.			
RA Kim C.J., Chen H., Cheuk R., Shim P., Ecker J.R.;			
RT "Arabidopsis ORF clones."			
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AL162875; CAB85555.1; -; Genomic_DNA.			
DR EMBL; BT021123; AAX2258.1; -; mRNA.			
DR PIR; T48445; T48445.			
DR GO; GO:0016020; C:membrane; IEA.			
DR GO; GO:004605; F:phosphatidate cytidyllyltransferase activity; IEA.			
DR GO; GO:008654; P:phospholipid biosynthesis; IEA.			
DR InterPro; IPR00374; PC_trans.			
DR Pfam; PF01148; CTP_transf_1.			
DR Hypothetical protein.			
SK SEQUENCE 304 AA; 33089 MW; 770CA569C9F50A50 CRC64;			

Query Match	100.0%;	Score 1536;	DB 2;	Length 304;
Best Local Similarity	100.0%;	Pred. No. 7.9e-112;		
Matches 304;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MAATLPSPIHQCRGNMSTTHRCSPGFLISSPCFGLTGMGATQURARRSLISS	60
DB	1	MAATLPSPIHQCRGNMSTTHRCSPGFLISSPCFGLTGMGATQURARRSLISS	60
QY	61	AAATNSLHDVGAAVVAATGGAVALVSPESITKKNVIOQSISRLGVNHSGLVFLAMP	120
DB	61	AAATNSLHDVGAAVVAATGGAVALVSPESITKKNVIOQSISRLGVNHSGLVFLAMP	120
QY	121	FGSGTEARVFAAPVLVNGRLVINGLSISPSNMLISVTRERABELLKGPLFYVIAL	180

Db 121 FSGSTEARYFAFVPLVNGRLVINGLSISPSNMLIKSVTREGRAEELLKGPLFYVALLL 180
Qy 181 FSAVFFMRBESPFGMISLAMCGGDIADIMGRKFGSTKIPNPRKSWAGSISMFIKGFPI 240
Db 181 FSAVFFMRBESPFGMISLAMCGGDIADIMGRKFGSTKIPNPRKSWAGSISMFIKGFPI 240
Qy 241 STALLYYSSIGYLIHMNETTLQRYAVMSVATVVESELPITDQDDNISVPLATILAAVL 300
Db 241 STALLYYSSIGYLIHMNETTLQRYAVMSVATVVESELPITDQDDNISVPLATILAAVL 300
Qy 301 SFGY 304
Db 301 SFGY 304

RESULT 2

Q84WC0 ARATH PRELIMINARY; PRT; 304 AA.
ID Q84WC0 ARATH PRELIMINARY; PRT; 304 AA.
AC Q84WC0;
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein At5g04490.
GN Name=At5g04490;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsids.
OK NCBI_TaxID=3702;
RN NUCLEOTIDE SEQUENCE.
RP Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamura A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shim P.,
RA Southwick A., Trimp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

RL EMBL; BT004006; AA042044.1; -, mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004605; F:phosphatidate cytidyltransferase activity; IEA.
DR GO; GO:0008654; P:phospholipid biosynthesis; IEA.
DR InterPro: IPR000374; PC:trans.
DR Pfam: PF01148; CTP transf_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 304 AA; 33059 MW; 361DBFC3635FA7FB CRC64;

Query Match 99.7%; Score 1531; DB 2; Length 304;
Best Local Similarity 99.7%; Pred. No. 1.9e-111;
Matches 303; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAATPLSPINHQLCRFGNNSLTTHRFCSPEGLISSPCFGLTGWGSATQLRARSLISS 60
Db 1 MAATPLSPINHQLCRFGNNSLTTHRFCSPEGLISSPCFGLTGWGSATQLRARSLISS 60
Qy 61 AATNSLHDVGATVAVVGAYALVLSPESTLTKRNVIOQSLSRKLVHLSGLFVLAMP 120
Db 61 AATNSLHDVGATVAVVGAYALVLSPESTLTKRNVIOQSLSRKLVHLSGLFVLAMP 120
Qy 121 FSGSTEARYFAFVPLVNGRLVINGLSISPSNMLIKSVTREGRAEELLKGPLFYVALLL 180
Db 121 FSGSTEARYFAFVPLVNGRLVINGLSISPSNMLIKSVTREGRAEELLKGPLFYVALLL 180
Qy 181 FSAVFFMRBESPFGMISLAMCGGDIADIMGRKFGSTKIPNPRKSWAGSISMFIKGFPI 240
Db 181 FSAVFFMRBESPFGMISLAMCGGDIADIMGRKFGSTKIPNPRKSWAGSISMFIKGFPI 240
Qy 241 STALLYYSSIGYLIHMNETTLQRYAVMSVATVVESELPITDQDDNISVPLATILAAVL 300
Db 241 STALLYYSSIGYLIHMNETTLQRYAVMSVATVVESELPITDQDDNISVPLATILAAVL 300

Qy 301 SFGY 304
Db 301 SFGY 304

RESULT 3

Q8LF61 ARATH PRELIMINARY; PRT; 304 AA.
ID Q8LF61 ARATH PRELIMINARY; PRT; 304 AA.
AC Q8LF61;
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsids.
OK NCBI_TaxID=3702;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22088475; PubMed=12093376;
RX Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY085036; AA061593.1; -, mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004605; F:phosphatidate cytidyltransferase activity; IEA.
DR GO; GO:0008654; P:phospholipid biosynthesis; IEA.
DR InterPro: IPR000374; PC:trans.
DR Pfam; PF01148; CTP transf_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 304 AA; 33069 MW; 937B18D809F3A626 CRC64;

Query Match 99.2%; Score 1523; DB 2; Length 304;
Best Local Similarity 98.7%; Pred. No. 8.2e-111;
Matches 300; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAATPLSPINHQLCRFGNNSLTTHRFCSPEGLISSPCFGLTGWGSATQLRARSLISS 60
Db 1 MAATPLSPINHQLCRFGNNSLTTHRFCSPEGLISSPCFGLTGWGSATQLRARSLISS 60
Qy 61 AATNSLHDVGATVAVVGAYALVLSPESTLTKRNVIOQSLSRKLVHLSGLFVLAMP 120
Db 61 AATNSLHDVGATVAVVGAYALVLSPESTLTKRNVIOQSLSRKLVHLSGLFVLAMP 120
Qy 121 FSGSTEARYFAFVPLVNGRLVINGLSISPSNMLIKSVTREGRAEELLKGPLFYVALLL 180
Db 121 FSGSTEARYFAFVPLVNGRLVINGLSISPSNMLIKSVTREGRAEELLKGPLFYVALLL 180
Qy 181 FSAVFFMRBESPFGMISLAMCGGDIADIMGRKFGSTKIPNPRKSWAGSISMFIKGFPI 240
Db 181 FSAVFFMRBESPFGMISLAMCGGDIADIMGRKFGSTKIPNPRKSWAGSISMFIKGFPI 240
Qy 241 STALLYYSSIGYLIHMNETTLQRYAVMSVATVVESELPITDQDDNISVPLATILAAVL 300
Db 241 STALLYYSSIGYLIHMNETTLQRYAVMSVATVVESELPITDQDDNISVPLATILAAVL 300
Qy 301 SFGY 304
Db 301 SFGY 304

RESULT 4

Q7KR51 ORYSA PRELIMINARY; PRT; 314 AA.
ID Q7KR51 ORYSA PRELIMINARY; PRT; 314 AA.
AC Q7KR51;

DT 01-OCT-2003 (TReMBLrel. 25, Created)
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE OSUNB0043A12.34 protein.
 GN Name=OSUNB0043A12.34;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriacaceae; Oryzae; Oryza.
 NCBI_TaxID=399477;
 RX NUCLEOTIDE SEQUENCE.
 RX PubMed:12447439; DOI=10.1038/nature01183;
 RA Feng Q., Zhang Y., Hao P., Wang S., Pu G., Huang Y., Li Y., Zhu J.,
 Li Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
 Wang Q., Zhang L., Lu Y., Mu Y., Lu Y., Zhang L.S., Yu Z., Fan D.,
 Lu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
 Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
 Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
 Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
 Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
 Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
 Han B.;
 RT "Sequence and analysis of rice chromosome 4.";
 RL Nature 420:316-320(2002).
 DR EMBL; AL606619; CAB02829.1; -; Genomic_DNA.
 DR Gramene; Q7X851; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004605; P:phosphatidate cytidyllyltransferase activity; IEA.
 DR GO; GO:0008654; P:phospholipid biosynthesis; IEA.
 DR InterPro; IPR000374; PC_trans.
 DR Pfam; PF01148; CTP_transf_1; 1.
 SQ SEQUENCE 314 AA; 33391 MW; 97B941B926576CF8 CRC64;
 Query Match 51.5%; Score 791.5; DB 2; Length 314;
 Best Local Similarity 51.1%; Pred. No. 1.2e-53;
 Matches 159; Conservative 60; Mismatches 81; Indels 11; Gaps 4;
 QY 2 AATPLPSINQLCR---FGNNSL---TTRFGSGRLISSPCTIGT-GKSGATQQLRA 53
 DB 3 AAAPFVDVRRPFCSSSVAASSSLISRSKSLASPAAMASMKRRRLVLGVGAAA--A 59
 QY 54 RRLSSAVATNSLHDVCAVAVGAVYALVSPESLTGKNVIOQSRLVHLISGL 113
 DB 60 PAVAAALASATPAALRDCAATLLITAGAYSLVRAADGLTARLLLEONSRKIVHLSGL 119
 QY 114 FYVALPFSGSTEARFAAFVPLVNGRLVINGLISFNSMLIKSVTEGRAEELKGPL 173
 DB 120 FMSWMPFNSNSTEARFAAIVPLNCRILVLYGLRLSTDALVSVTEGKPEBELRGPL 179
 QY 174 FYVALPFSAVFPMRESPIGIMISLAMCGGDIADINGRKRTGTYKIPNPKSMAAGISL 233
 DB 180 YVYVLLVSVVLPFRQSPIGIVSLSMGSGDGFADIVGRYGSALPFPENKMSWIGISL 239
 QY 234 FIFGFEPIALLYYSSIGYLMNMETTLORVAVSMVATVSESPIPDOLDNNISVLA 293
 DB 240 FIFGFEPIALLYYSSIGYLMNMETTLORVAVSMVATVSESPIPDOLDNNISVLA 299
 QY 294 TILAAYLSFGY 304
 DB 300 TMLAAVLLFGY 310
 RESULT 5
 Q5N9J9_ORYZA PRELIMINARY; PRT; 246 AA.
 AC Q5N9J9;
 DT 01-FEB-2005 (TReMBLrel. 29, Created)
 DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
 DE Hypothetical protein P0446G04.41.
 GN Name=P0446G04.41;
 OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriacaceae; Oryzae; Oryza.
 NCBI_TaxID=399477;
 RX NUCLEOTIDE SEQUENCE.
 RX Saeki T., Matsuno T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
 RA Hosokawa S., Maekawa M., Arikawa K., Chiden Y., Hayashi M.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
 RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
 RA Katsawa W., Katsagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
 RA Nagasaki K., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Nankai N., Negishi M., Ohta I., Ono N., Sai S., Sakai K., Shibata M.,
 RA Shimokawa T., Shomura A., Song J., Takasaki Y., Teraawa K., Teuji K.,
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshitake R., Yukawa K.,
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Bun M.Y.,
 RA Yano M., Jiang J., Gojobori T.;
 RT "The genome sequence and structure of rice chromosome 1.";
 RL Nature 420:312-316(2002).
 DR EMBL; AP003252; BAB1857.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004605; P:phosphatidate cytidyllyltransferase activity; IEA.
 DR GO; GO:0008654; P:phospholipid biosynthesis; IEA.
 DR InterPro; IPR000374; PC_trans.
 DR Pfam; PF01148; CTP_transf_1; 1.
 DR Hypothetical protein.
 SQ SEQUENCE 246 AA; 26457 MW; F830AB7300BE24E8 CRC64;
 Query Match 36.8%; Score 565.5; DB 2; Length 246;
 Best Local Similarity 44.5%; Pred. No. 4.1e-36;
 Matches 106; Conservative 47; Mismatches 84; Indels 1; Gaps 1;
 QY 65 NSLHDVCAVAVGAVYALVSPESLTGKNVIOQSRLVHLISGLFYLAAPFSGS 124
 DB 10 SGLAHDSAAVAVTGVALALRPFELAKGVFPQKRLKVLHTIGVPLFLPPLFSSG 69
 QY 125 TEATFAAFVPLVNGRLVINGLISFNSMLIKSVTEGRAEELKGPLFYVALLES 184
 DB 70 SYAPPLAAVAPGINIIRLLGLGVNKEAMVKSMSRSGDREBLKGPLYATITTFATS 129
 QY 185 FPMRESPIGIMISLAMCGGDIADINGRKRTGTYKIPNPKSMAAGISL 244
 DB 130 IFWRTSPALALNCLAGDIADIVGRIGQELPYNPKSVYGSILAMALAGFMAISGY 189
 QY 245 LYYSSIGYLMNMETTLORVAVSMVATVSESPIPDOLDNNISVLA 302
 DB 190 MHYFQSGFIFESNSLAF-GLVAVSVTALVESHPISTHLDNLTVPILTSVLSVIF 246
 RESULT 6
 Q67ZW7_ARATH PRELIMINARY; PRT; 307 AA.
 AC Q67ZW7;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DE Hypothetical protein At5g58560.
 GN Name=At5g58560;
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 RX NUCLEOTIDE SEQUENCE.
 RX Tsuchi Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
 RA Narusaka M., Shin-I T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
 RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
 RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinzeki K.;

RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs."
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK176090; BAD43853.1; -; mRNA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004605; F:phosphatidate cytidyltransferase activity; IEA.
 DR GO: GO:0008654; P:phospholipid biosynthesis; IEA.
 DR InterPro: IPR000374; PC:trans.
 DR Pfam: PF01148; CTP transf_1; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 307 AA; 33204 MW; 598BB448D4450C1F CRC64;

Query Match 34.6%; Score 531.5; DB 2; Length 307;
 Best Local Similarity 38.1%; Pred. No. 2.4e-33;
 Matches 120; Conservative 66; Mismatches 108; Indels 21; Gaps 7;

QY 1 MAATLPSPINHQCRFGNSLTTRFCSP---GFLISSPCFGL---TGMSATQLRAR 54
 DB 1 MATSTTKLSVLCSSFISSPLVD---SPSLAFSPPIRFLVRIATSRSSSRPAT 56
 QY 55 RSLISSAVAT---NSLHADV---GATVAVLGAYALVLSFESLTGRNVIOQSIRKLVH 107
 DB 57 KIRSSSLAAVWPENSVLSDVCAGVTSIV---AFSCIGFWEIGIKRGIIPQKILRKLVH 113
 QY 108 ILSGLFLVLAAMPFSGSTEARYPAAFPVLVNGLRVLVNGLSISNSMLIKSVTEGRAAE 167
 DB 114 INIGLVFMLCWPFLFSSGIGQALFASLVPGLVNIVRMILLGLGVYHDEGTIKMSRRGRRE 173
 QY 168 LKGGPLVYVLAALFSAVFFWRFPSPIGMISLMMCGGDGIADIMGRKFGSTKIPNPRKSF 227
 DB 174 LKGGPLVYVLAALFSAVFFWRFPSPIGMISLMMCGGDGIADIMGRKFGSTKIPNPRKSF 233
 QY 228 AGSISMFIFGFISIALYYSLSGLYLMNMWETTLQRYAVMSVATVESLPITDQDND 287
 DB 224 AGSISMAFAGFLASVAVMYVYFASFGYIEDSGMIL-RFLVISIASALVESLPISTDIDN 292
 QY 288 ISVPLATILAAVLSF 302
 DB 293 LTISLTSALAGFLF 307

RESULT 7
 Q672A1 ARATH PRELIMINARY; PRT; 307 AA.
 AC Q672A1;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 GN Hypothetical protein At5g358560.
 GN Name=At5g358560;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxId=3702;
 RN NM
 RP NUCLEOTIDE SEQUENCE.
 RA Tsuchida Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
 RA Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
 RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
 RA Satou M., Toyoda T., Kanagaya A., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinozaki K.;
 RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs."
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK176217; BAD43980.1; -; mRNA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004605; F:phosphatidate cytidyltransferase activity; IEA.
 DR GO: GO:0008654; P:phospholipid biosynthesis; IEA.
 DR InterPro: IPR000374; PC:trans.
 DR Pfam: PF01148; CTP transf_1; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 307 AA; 33218 MW; F98BB457D44D1079 CRC64;

Query Match 34.5%; Score 530.5; DB 2; Length 307;

Best Local Similarity 37.8%; Pred. No. 2.8e-33;
 Matches 119; Conservative 67; Mismatches 108; Indels 21; Gaps 7;

QY 1 MAATLPSPINHQCRFGNSLTTRFCSP---GFLISSPCFGL---TGMSATQLRAR 54
 DB 1 MATSTTKLSVLCSSFISSPLVD---SPSLAFSPPIRFLVRIATSRSSSRPAT 56
 QY 55 RSLISSAVAT---NSLHADV---GATVAVLGAYALVLSFESLTGRNVIOQSIRKLVH 107
 DB 57 KIRSSSLAAVWPENSVLSDVCAGVTSIV---AFSCIGFWEIGIKRGIIPQKILRKLVH 113
 QY 108 ILSGLFLVLAAMPFSGSTEARYPAAFPVLVNGLRVLVNGLSISNSMLIKSVTEGRAAE 167
 DB 114 INIGLVFMLCWPFLFSSGIGQALFASLVPGLVNIVRMILLGLGVYHDEGTIKMSRRGRRE 173
 QY 168 LKGGPLVYVLAALFSAVFFWRFPSPIGMISLMMCGGDGIADIMGRKFGSTKIPNPRKSF 227
 DB 174 LKGGPLVYVLAALFSAVFFWRFPSPIGMISLMMCGGDGIADIMGRKFGSTKIPNPRKSF 233
 QY 228 AGSISMFIFGFISIALYYSLSGLYLMNMWETTLQRYAVMSVATVESLPITDQDND 287
 DB 224 AGSISMAFAGFLASVAVMYVYFASFGYIEDSGMIL-RFLVISIASALVESLPISTDIDN 292
 QY 288 ISVPLATILAAVLSF 302
 DB 293 LTISLTSALAGFLF 307

RESULT 8
 Q8LAW9 ARATH PRELIMINARY; PRT; 307 AA.
 AC Q8LAW9;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 GN Hypothetical protein. (Mouse-ear cress).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxId=3702;
 RN NM
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22088475; PubMed=12093376;
 RA Haas B.J., Volfovsky N., Town C.D., Troupkhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 annotation."
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029 (2002).
 RN NM
 RP NUCLEOTIDE SEQUENCE.
 RA Brover V., Troupkhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY087555; AA065097.1; -; mRNA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004605; F:phosphatidate cytidyltransferase activity; IEA.
 DR GO: GO:0008654; P:phospholipid biosynthesis; IEA.
 DR InterPro: IPR000374; PC:trans.
 DR Pfam: PF01148; CTP transf_1; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 307 AA; 33204 MW; F98BB251D44B1679 CRC64;

Query Match 34.3%; Score 526.5; DB 2; Length 307;
 Best Local Similarity 37.5%; Pred. No. 5.8e-33;
 Matches 118; Conservative 67; Mismatches 109; Indels 21; Gaps 7;

QY 1 MAATLPSPINHQCRFGNSLTTRFCSP---GFLISSPCFGL---TGMSATQLRAR 54
 DB 1 MATSTTKLSVLCSSFISSPLVD---SPSLAFSPPIRFLVRIATSRSSSRPAT 56
 QY 55 RSLISSAVAT---NSLHADV---GATVAVLGAYALVLSFESLTGRNVIOQSIRKLVH 107

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Db 57 KIRKSLAAMFPENSVDVCAFGVTSIV--AFSCIFGWEIGKRGIFPOKLRKLVH 113
Qy 108 ILGLFLVLAAMPFGSGTEARFAFVPLVNLGRLVINGLSRPSMLIKSTREGRABE 167
Db 114 INIGIVFLCWPFLFSSGIGQALFASLVPGLNIVRLGLGVYHDEGTIKSMRGRDRE 173
Qy 168 LKGLFLVLAALFSAVFWRSPYGMISLMMCGGDDIADIMGRKFGSTKIPYPRKSW 227
Db 174 LKGLFLVLAALFSAVFWRSPYGMISLMMCGGDDIADIMGRKFGSTKIPYPRKSW 233
Qy 228 AGSISMPFGEFFISIALIYSSIGLYLHMNETTLQRYAMVSVATVESLPITDOLDN 287
Db 234 AGSISMPFGEFFISIALIYSSIGLYLHMNETTLQRYAMVSVATVESLPITDOLDN 292
Qy 288 ISVPLATLAAVLSF 302
Db 293 LTSLTSLAGPLLF 307

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RESULT 9

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Q9LV00 ARATH PRELIMINARY; PRT; 517 AA.
AC Q9LV00;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Emb|CAB8555.1.
OS Arabidopsis thaliana (mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustosida II; Brassicales; Brassicaceae; Arabidopsids.
CX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and IAC
RT clones";
RL DNA Rep. 7:31-63(2000).
DR EMBL; AB020755; BAA97326.1; -; Genomic DNA.
SQ SEQUENCE 517 AA; 56646 MW; 85D803CE7688BE8A CRC64;

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Query Match 29.7%; Score 455.5; DB 2; Length 517;
 Best Local Similarity 37.1%; Pred. No. 3.5e-27;
 Matches 106; Conservative 59; Mismatches 100; Indels 21; Gaps 7;

```

Qy 1 MAATLPLSPINHQCRFGNNSLTTRFCSP---GFLISSPCIGL---TGMSATQLAR 54
Db 1 MATSTTTKLSVLCSSFISSPLVD---SPSLAFSPFIPRLTVRIATSRSSSRFPAT 56
Qy 55 RSLISSAVAT---NSLIHVV---GATVAVLGAVAVLVSFESLTKRNVIOQSRLKLVH 107
Db 57 KIRKSLAAMFPENSVDVCAFGVTSIV--AFSCIFGWEIGKRGIFPOKLRKLVH 113
Qy 108 ILGLFLVLAAMPFGSGTEARFAFVPLVNLGRLVINGLSRPSMLIKSTREGRABE 167
Db 114 INIGIVFLCWPFLFSSGIGQALFASLVPGLNIVRLGLGVYHDEGTIKSMRGRDRE 173
Qy 168 LKGLFLVLAALFSAVFWRSPYGMISLMMCGGDDIADIMGRKFGSTKIPYPRKSW 227
Db 174 LKGLFLVLAALFSAVFWRSPYGMISLMMCGGDDIADIMGRKFGSTKIPYPRKSW 233
Qy 228 AGSISMPFGEFFISIALIYSSIGLYLHMNETTLQRYAMVSVATVESLPITDOLDN 287
Db 234 AGSISMPFGEFFISIALIYSSIGLYLHMNETTLQRYAMVSVATVESLPITDOLDN 292

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RESULT 10
 Q86HK6 D1CD1 PRELIMINARY; PRT; 1144 AA.
 AC Q86HK6;

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DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Similar to Oryza sativa (Japonica cultivar-group). P04460.23 protein
DE (Fragment).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
CX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J.A.,
RA Barkley A.T., Dear P.H., Lehmann R., Baumgart C., Parra G.,
RA Abriol J.P., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A.,
RA Platzner M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum";
RL Nature 418:79-85(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116989; AAO52579.2; -; Genomic DNA.
FT NON TER 1 1
SQ SEQUENCE 1144 AA; 128163 MW; 748CFD3A53433730 CRC64;

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Query Match 20.1%; Score 309.5; DB 2; Length 1144;
 Best Local Similarity 29.4%; Pred. No. 2.1e-15;
 Matches 90; Conservative 56; Mismatches 107; Indels 53; Gaps 11;

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Qy 20 NSLTHRCSPGFLISSPCIFGLTGMGSAHQRLARRSLISSAVATNSLIHVGATVAVLG 79
Db 871 NSLWNSNFSSTIKFYTSN-----NLDHLENNKTTISNSGTTIN-----GCQVSTKS 914
Qy 80 GAVAVLSFESLITR-----NVIQGLSRGLVLIISGLFLVLAAMPF-SGST 125
Db 915 GHKSMALFNSCMERKSIPTVYTFISAVGVCIQL---LHIGGIIVLVYMRFPQCNW 971
Qy 126 EARYFAFVPLVNLGRLVINGLSRPSMLIKSTREGRABELKGLFLVLAALFSAVF 185
Db 972 YSKIVGVLPVLIISFYQVALIGLIINDQKTVESMSRSGSPRELLGFLSYGIITSLTMI 1031
Qy 186 FWRSPYGMISLMMCGGDDIADIMGRKFGSTKIPYPRKSMASISMF---FGFISI 242
Db 1032 FW-RSPYISITIGVLCGDFALFGLKYGKRIPIYRREKTLISLAFICSTIGFTLL 1090
Qy 243 AL-----LYYSSIGLYLHMNETTLQRYAMVSVATVESLPITDOLDNISVPLATIAA 298
Db 1091 TLDDRLIYPSIVLAPSLF-----VCLISTLISLPRLDW--DNITISICSVITL 1139
Qy 299 YLSFGY 304
Db 1140 NL-MGY 1144

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RESULT 11
 Q55A10 D1CD1 PRELIMINARY; PRT; 223 AA.
 AC Q55A10;
 DT 13-SEP-2005 (Tremblrel. 31, Created)
 DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
 DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=DD80216976;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 CX NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
 RA Sugeng R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,

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RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Plicher K., Chen G., Saunders D., Sodergren E., Davis P., Bason N.,
RA Kethornou A., Nie X., Hall N., Angard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Mundy D., Mourier T., Pain A., Lu M., Harper D., Linday R.,
RA Hauser H., James K., Quiles M., Mohan B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louised H., Mungall K., Oliver K., Price C., Quail M.A., Sanders M.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmons M., Spiegler S., Tiley A.,
RA Sueno S., White B., Walker D., Woodward J., Winkler T., Tanaka Y.,
RA Shuley G., Schlicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Glibbe R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kasper A.,
RT "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 0:0-0(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC DR EMBL; AAF0100020; EAL71342.1; -; Genomic_DNA.
CC KW Hypothetical protein.
SQ SEQUENCE 223 AA; 25192 MW; 83AB36930DF15C26 CRC64;

Query Match 18.6%; Score 285; DB 2; Length 223;
Best Local Similarity 33.2%; Pred. No. 3e-14; Indels 22; Gaps 8;
Matches 76; Conservative 44; Mismatches 97;

QY 84 LVLSFESLTKRVNIQOOSLSRKLVIHLSGLFVLAAMPF-SGSTEARPAFVPLVNGRL 142
DB 9 LTLSTVICLMWMLNFCQFLKKHKVTS-STGIIVLVWRIFQFWYRSIVGLVPLISPOY 67
QY 143 VINGISISPSNMLISVTRGAEELKLPFLVYVALLFSAVFFRSPISGISMAMCG 202
DB 68 ALIGGIINDQKTVSMRSGSPRELLGPIISYGIISLITWIFW-FSPISITITGVCL 126
QY 203 GGGIINDIMGRKSGSKIPYNPSPKSWAGSISMT---FGPFSIAL---LYYSSISGLYH 255
DB 127 GGGPAIFELKTKYKIPNREKTIIGSLAFLFCIFGFIITLLOBLRYPSTIVLAP 186
QY 256 NMWETTLQVAMVAMATVWESLPTTDQDNIISVPLATIIAIVLSFGY 304
DB 187 LFW-----VCLISTIEISLPLRDM--DNITTSISGVLTNLN-MGY 223

RESULT 12
OS06D6 ENTHI PRELIMINARY; PRT; 228 AA.
ID OS06D6 ENTHI PRELIMINARY;
AC OS06D6_
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=382.C00006;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RA PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Almark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Bettman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leipzig M.,
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Slicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Frazer C.M., Hall N.;

```

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RT "The genome of the protist parasite Entamoeba histolytica."
RL Nature 433:865-868(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC DR EMBL; AAFB01005976; EAL3455.1; -; Genomic_DNA.
CC KW Hypothetical protein.
SQ SEQUENCE 228 AA; 25935 MW; 95BE1A30092FD159 CRC64;

Query Match 16.7%; Score 257; DB 2; Length 228;
Best Local Similarity 32.9%; Pred. No. 4.8e-12; Indels 16; Gaps 8;
Matches 68; Conservative 44; Mismatches 79;

QY 97 IQOSLSRKLVIHLSGLFVLAAMPFSGSTEARPAFVPLVNGRLVINGL--SISPSNM 154
DB 30 LQGSISRKLTLHLGPFILTWKRYPTSLSCYIAATPLPSISILLFCYLFQKLSIQF 89
QY 155 LKSVTRGAEELKLPFLVYVALLFSAVFFRSPISGISMAMCGGDIADIMGRK 214
DB 90 IIQISHNKEPHELEBPFIYGVVISLITWLFWDTPVGIIISIIILGIDGMADIIGSL- 148
QY 215 GSTKIPNP--RKSMAGSISMTFGPFSIALYLYSSISGLYHNMWETTLQVAMVAMVA 272
DB 149 -STVIVPAFGRKTFDCCS-FIFPSFICGVFEYI---IFRQIW--ILNTIAIVSL-G 199
QY 273 TVVESLPTDQDNIISVPLATIIAIV 299
DB 200 CTFEF--ISPLFPNLTITLTSTIAF 224

RESULT 13
OS06G1 ENTHI PRELIMINARY; PRT; 230 AA.
ID OS06G1 ENTHI PRELIMINARY;
AC OS06G1_
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=189.C00015;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RA PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Almark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Bettman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leipzig M.,
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Slicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Frazer C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica."
RL Nature 433:865-868(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC DR EMBL; AAFB01005976; EAL45593.1; -; Genomic_DNA.
CC KW Hypothetical protein.
SQ SEQUENCE 230 AA; 25686 MW; 64960D19C80E3C08 CRC64;

Query Match 16.0%; Score 245.5; DB 2; Length 230;
Best Local Similarity 26.6%; Pred. No. 3.8e-11; Indels 37; Gaps 6;
Matches 61; Conservative 51; Mismatches 80;

QY 90 SITKENVIQOOSLSRKLVIHLSGLFVLAAMPFSGSTEARPAF-----FVPLVNGRL 142
DB 23 ALSKNITITSYRSKIVHISLGVCIIVMGCYSEPTARIWGSICCILYFLFVFLIFGMGW 82

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QY 143 VINGLISPNMILKSVTRBGRABELLKGPLFYVALLFSAVFWRSPISGIMISLAWMG 202
 DB 83 IKGP1A-----DPLATVCRNGDYKEMLYGPLNYCCIMFPLSLWRYNPASTIGMILMT 138
 QY 203 GDGIADIWGRKFGSTKI--PYNPRKSWAGSISMFIFG-----FFISIALLYYSISGY 253
 DB 139 GDGMAEIIKGMIGKTLQKNPCKTKTIGALAVWCGAVGMWVCYIIIFGQIFIGSI-- 196
 QY 254 LHMWETTLQRVAVMSVATVYESIPTDQLDNISVPLATITLAAYLSF 302
 DB 197 -----ISGLVGAIVEFYSPYNY--DNVFIPLSSILLGFFIF 230

RESULT 14
 Q8KB08_CHLITE PRELIMINARY; PRT; 237 AA.
 AC Q8KB08;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS OrderedLocustNames=CT1990;
 GN Chlorobium tepidum.
 OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
 OC Chlorobaculum.
 NCBI_TaxID=1097;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JLS / ATCC 49652 / DSM 12025;
 RX MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;
 RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
 Raeborn R.J., Deboy R.T., Gwim M.L., Nelson W.C., Holt D.H.,
 Hekey E.K., Peterson J.D., Durkin A.S., Kolony J.F., Yang F.,
 Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,
 Raskes D.S., Nierman W.C., Feldblum T.V., Hansen C.L., Craven M.B.,
 Radune D., Vamathevan J.J., Knouri H.M., White O., Gruber T.M.,
 R. Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
 RT "The complete genome sequence of Chlorobium tepidum JLS, a
 photoautotrophic, anaerobic, green-sulfur bacterium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
 DR EMBL; AB006470; AAM73208.1; -; Genomic_DNA.
 DR TIGR; CT1990; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004605; F:phosphatidate cytidyltransferase activity; IEA.
 DR GO; GO:0008654; P:phospholipid biosynthesis; IEA.
 DR InterPro; IPR000374; PC:trans.
 DR Pfam; PF01148; CTP transf. 1; 1.
 DR Complete proteome; Hypothetical protein.
 SQ SEQUENCE 237 AA; 25945 MW; 4211926508BEE71 CRC64;

Query Match 15.2%; Score 234; DB 2; Length 237;
 Best Local Similarity 27.2%; Pred. No. 3.1e-10;
 Matches 65; Conservative 58; Mismatches 92; Indels 24; Gaps 7;

QY 69 HDVGATVAVLGGATVAVLSPESLTKRNVIOQSLSKLVHIIISGLLFVLAWIFSGSTAR 128
 DB 16 HNVAVMLLTITVYVSVPLMDMLVTNGLPRDISKIRHICAGSVYPL-PLFRDGMWSH 74
 QY 129 YFAFVPLVNLGRVINGLISPNMILKSVTRBGRABELLKGPLFYVALLFSAVFWR 188
 DB 75 YLNTVPAVTVVTLIQKLPFAADDAVKTMTCTGDKRELKGPLFYVAVMIGCTLYK 134
 QY 189 ESPIGMISLAWMGCGDIADIMGRKFGSTKI-PYNPRKSWAGSISMFIFG-----FFISI 242
 DB 135 QF-AGVILAMAILGWDGLAPIVGTBMGMKVKVFCERSVEGSLA-FLAGSLAAGLFFVWL 192
 QY 243 ALITYYSSGLYHNMWETTLQRVAVMSVATVYESIPTDQLDNISVPLATI-LAAVL 300
 DB 193 IVPAQFND-----AKIAMIAVAATVIEAL--SPKVDNITLPAEVIALAAVL 237

RESULT 15

050LM4_ENTHI
 ID Q50LM4_ENTHI PRELIMINARY; PRT; 230 AA.
 AC Q50LM4;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=687.t00002;
 OS Entamoeba histolytica HM-1:IMSS.
 OC Eukaryota; Entamoebidae; Entamoeba.
 NCBI_TaxID=294381;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HM-1:IMSS;
 RX PubMed=15729342; DOI=10.1038/nature03291;
 RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
 Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
 Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
 Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
 RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
 Jagers K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
 Quail M.A., Rabinowitz E., Norbertczak H., Price C., Wang Z.,
 RA Guillen N., Gilchrist C., Stroup S.B., Bhattacharya S., Lohia A.,
 RA Foster P.G., Sierichitz-Ponten T., Weber C., Singh U., Mukherjee C.,
 RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
 RA Fraser C.M., Hall N.;
 RT "The genome of the eucariotic parasite Entamoeba histolytica.";
 RL Nature 433:865-868 (2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABP01001460; EML42582.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 230 AA; 25851 MW; E7F78A75787B56D7 CRC64;

Query Match 15.0%; Score 230; DB 2; Length 230;
 Best Local Similarity 26.5%; Pred. No. 6.2e-10;
 Matches 67; Conservative 49; Mismatches 97; Indels 40; Gaps 7;

QY 59 SSAVATNSLHDVGATVAVLGGATVAVLSPESLTKRNVIOQSLSKLVHIIISGLLFVLAW 118
 DB 9 TSLAVNVCL--IATL-----LSKTNIIITSYTSRKKCVHISLGFOLLW 51
 QY 119 PIFSGTEARFPAFVPLVNLGRVINGLISPNMILKSVTRBGRABELLKGPLFY 175
 DB 52 KYEPEPTARIWGMCCILYAIVFLFGMKIKGVADPLATVCRNGDYKEMLYGPLNY 111
 QY 176 VLLAFSAVFWRSPISGIMISLAWMGCGDIADIMGRKFGSTKI--PYNPRKSWAGSISM 233
 DB 112 CIMSFSLSLWRYNPSSIIIGAMVMLTGDMAEIIKGMIGKTLQKNPCKTKTIGEAIV 171
 QY 234 FIFGFFISIALLYYSISGLYHNMWETTLQRVAVMSVATVYESIPTDQLDNIS 289
 DB 172 MVCG-----SLGAMFMCMLFNNFYIIESIVGFGVAIVEFYCPNY--DNVF 217
 QY 290 VPLATITLAAYLSF 302
 DB 218 IPLSSVWGAIFF 230

Search completed: March 16, 2006, 19:51:00
 Job time : 115 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 16, 2006, 19:51:15 ; Search time 29 Seconds

(without alignments)
866.669 Million cell updates/sec

Title: US-10-634-548-2

Perfect score: 1536

Sequence: 1 MAATLPLSPINHQCRCFGNN.....DDNISVPLATILAAVLSFGY 304

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/PC/US_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105.5	6.9	164	2	US-09-248-796A-16153 Sequence 16153, A
2	100.5	6.5	285	2	US-09-328-352-7257 Sequence 7257, Ap
3	100.5	6.5	296	2	US-09-540-236-2118 Sequence 2118, Ap
4	99	6.4	515	2	US-09-328-352-5090 Sequence 5090, Ap
5	98.5	6.4	383	2	US-09-710-279-2168 Sequence 2168, Ap
6	98.5	6.4	452	2	US-09-134-001C-3935 Sequence 3935, Ap
7	97.5	6.3	300	2	US-09-543-681A-4454 Sequence 4454, Ap
8	97	6.3	431	2	US-09-549-848B-6 Sequence 6, Appl1
9	97	6.3	445	2	US-09-688-069-6 Sequence 6, Appl1
10	97	6.3	446	2	US-09-134-000C-6454 Sequence 6454, Ap
11	96	6.2	330	2	US-09-488-039A-10968 Sequence 10968, A
12	95	6.2	461	1	US-08-672-814D-2 Sequence 2, Appl1
13	95	6.2	461	1	US-09-333-696-2 Sequence 2, Appl1
14	95	6.2	461	2	US-09-282-218A-2 Sequence 2, Appl1
15	94.5	6.2	424	2	US-09-134-001C-5009 Sequence 5009, Ap
16	94	6.1	251	2	US-09-134-000C-4324 Sequence 4324, Ap
17	94	6.1	462	2	US-09-328-352-4694 Sequence 4694, Ap
18	93.5	6.1	409	2	US-09-710-279-2002 Sequence 2002, Ap
19	93.5	6.1	414	2	US-09-710-279-2306 Sequence 2306, Ap
20	93.5	6.1	409	2	US-09-489-039A-10869 Sequence 10869, A
21	93.5	6.1	662	1	US-07-841-651-4 Sequence 4, Appl1
22	93	6.1	308	2	US-09-328-352-7092 Sequence 7092, Ap
23	93	6.1	940	2	US-09-328-352-8165 Sequence 8165, Ap
24	92	6.0	538	2	US-09-107-532A-5563 Sequence 5563, Ap
25	91.5	6.0	542	2	US-09-605-703B-492 Sequence 492, App
26	91.5	6.0	688	2	US-09-605-703B-490 Sequence 490, App
27	91	5.9	516	2	US-09-949-016-11239 Sequence 11239, A

28	90	5.9	332	2	US-09-830-217-20 Sequence 20, Appl
29	90	5.9	332	2	US-10-278-946-20 Sequence 1993, Ap
30	89.5	5.8	444	2	US-09-540-236-1993 Sequence 1993, Ap
31	89.5	5.8	479	2	US-09-583-110-4687 Sequence 4687, Ap
32	89.5	5.8	480	2	US-09-107-433-3418 Sequence 3418, Ap
33	89	5.8	289	2	US-09-489-039A-12390 Sequence 12390, A
34	89	5.8	408	2	US-09-543-681A-4822 Sequence 4822, Ap
35	88	5.7	279	2	US-08-549-515-7 Sequence 7, Appl1
36	87.5	5.7	316	2	US-09-549-848B-33 Sequence 33, Appl
37	87.5	5.7	316	2	US-09-688-069-33 Sequence 33, Appl
38	87.5	5.7	348	2	US-09-543-681A-5845 Sequence 5845, Ap
39	87.5	5.7	397	2	US-09-602-787A-628 Sequence 628, App
40	87.5	5.7	629	2	US-09-602-787A-624 Sequence 624, App
41	87	5.7	423	2	US-09-328-352-6097 Sequence 6097, Ap
42	87	5.7	484	2	US-09-328-352-7797 Sequence 7797, Ap
43	87	5.7	544	2	US-09-902-540-16154 Sequence 16154, A
44	86.5	5.6	307	2	US-09-107-532A-6125 Sequence 6125, Ap
45	86	5.6	220	2	US-09-603-552-13 Sequence 13, Appl

ALIGNMENTS

```

RESULT 1
US-09-248-796A-16153
Sequence 16153, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Kelch Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 16153
LENGTH: 164
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-16153

Query Match      6.9%; Score 105.5; DB 2; Length 164;
Best Local Similarity 23.2%; Pred. No. 0.0004;
Matches 38; Conservative 35; Mismatches 66; Indels 25; Gaps 8;

QY 152 NSMLIKSVTGRREELKGPFLFYVALLFSVAFPMRESPIGMTSLMCGDGIADIMG 211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 NCSSWTSVVIDNDENYS-YNGTLFYLGVLT--VLVAVPKDISIVISILLSMADTPAASFP 58
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 212 RKFGSTRKIPYNR-----KSWAGSISMF1-----FGFFISIALLYYSSLGYLHMMW 258
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 RARPK-----YTPQASKSLAGCLASCVTGLTAYLYMGYF--IPQYNNMNPBEIYRNA 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 113 NSNGLSPVYSLIGVITSEVIDIADIDNFPVLSGTCY 156

RESULT 2
US-09-328-352-7257
Sequence 7257, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-039A
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04

```

```

; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7257
; LENGTH: 285
; TYPE: PRF
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7257

```

Query Match	6.5%	Score 100.5;	DB 2;	Length 285;
Best Local Similarity	21.2%;	Pred. No. 0.0037;		
Matches	48;	Conservative	40;	Mismatches 83;
			Indels	55;
			Gaps	8;

```

QY 70 VVGATVAVLGGAVYLVLPES---LTGKNVIGQSLSRKLVTHTLSGLFLFVLAIPISGSTE 126
   ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 61 EVGAVKRRKAMGYGLTVAFVSGVALFFHDIALMLASALITLTVAITYVAKSPFEDDKMTN 120

QY 127 ARYPAAFPVLYNGSLVINGLISISPSNMLIKSVTREGRAEELIKGPLFYVALLPASAFV- 185
   :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 121 ATLY-----YIGLILICAAV-----TALIV 140

QY 186 FWRBSPICMISLAWMC-GGDGIADIMGRKFGSTKI--PYNPKSWAGSISMTIFGFESISI 242
   :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 141 VMQSSPMMIMLYFLTLVWGADSGAVFVGKFKGKRLAPTVSPKSVSEG-----LYGILTT 195

QY 243 ALLYYSSSLGYLHMMWETTLQRYVAVSWAVATVESLPIFDQDDNNI 288
   ||| :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 196 IIVMLVVOYQYINLTW---VOOLPLILISLTVPQSVGLDLEPSMTI 238

```

```

, RESULT 3
, US-09-540-236-2118
, Sequence 2118, Application US/09540236
, Patent No. 6673910
, GENERAL INFORMATION:
, APPLICANT: Gary L. Breton et al.
, TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
, TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
, FILE REFERENCE: 2709 2005-001
, CURRENT APPLICATION NUMBER: US/09/540,236
, CURRENT FILING DATE: 2000-04-04
, NUMBER OF SEQ ID NOS: 3840
, SEQ ID NO 2118
, LENGTH: 296
, TYPE: prt
, ORGANISM: M.catarrhalis
, US-09-540-236-2118

```

Query Match	6.5%;	Score 100.5;	DB 2;	Length 296;
Best Local Similarity	27.0%;	Pred. No. 0.004;		
Matches	40;	Conservative	28;	Mismatches 51;
				Indels 29;
				Gaps 9;

```

QY      173 LEFYVALLFSAVP-----FWRESF--IGNISLAWCGGGIADIMOKRKGSGTFLPYN--P 223
Db      120 LYYMGAVILTAITANYGLMCMSPMWLVFLVWADSG-AFYIQRKSGKRRMAPNVP 178
QY      224 RKSNAGSTIMFLFGFPISTALLYYYSLSG-----YLAHNMETTLQRY-----AMVSVA 272
Db      179 NKSIEGLCGGLAVSGVYVAVGGYIQLSGSLVLFILISWLVLASIILADLFESMLKRR 238
QY      273 TVVES---LP-----ITDOLDNIS--VPL 292
Db      239 GKDGSGTILPGHGILRIDSLSLALPI 266

```

```

RESULT 4
US-09-328-352-5090
; Sequence 5090, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352

```

```

; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5090
; LENGTH: 515
; TYPE: PR1
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5090

```

Query Match	6.4%;	Score 99;	DB 2;	Length 515;
Best Local Similarity	24.6%;	Pred. No. 0.014;		
Matches 60;	Conservative 40;	Mismatches 94;	Indels 50;	Gaps 14;

```

QY      7 LSPINHCRCFENNBLTTRHFCSPGFLISSPCFIGL-TGMG---SATOL-----RARSH 57
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db     23 LNFIRKYKDESSASMINASVACVEQIVNEGRRAYGINQFGILLASTKXIAPEDEKIQRSI 82

QY      58 I-SSAVATNSLIHDGATVAIVGGAVALVLSPESLTKRNVIOOSL-----SRKLVH----- 108
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db     83 VLSHAGVGEALDDMMVRILILKKNSSLARGSGI-RRRYVDALLALINAEVYPHPLPLKG 141

QY      109 ---LSGLLFLVLAWP--IFSGSTEARYFAFVPLVNGLRVLVINGLSISPSMILIKSVTRREG 163
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db     142 SVGASGDPLAPLAHMSLVLLGESKARYKKGWMLRAVELKKA-----GLEPISLAHK-----BS 193

QY      164 RAEBLLKG---PLFYVALLLFSQAVEFWRESPIGMISLAMCGGDGIADIIMGRKFGSTKIP 220
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db     194 IAA-LINGQVSTAYALRGLFEAE-----DLFAATVACGGLSYEAMLG-----SRAP 238

QY      221 YNPR 224
      ::|

Db     239 FPAR 242

```

```

RESULT 5
US-09-710-279-2168
; Sequence 2168, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS4800S
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2168
;
; LENGTH: 383
;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
;
US-09-710-279-2168

```

Query Match	6.4%;	Score 98.5;	DB 2;	Length 383;
Best Local Similarity	19.9%;	Pred. No. 0.01;		
Matches 67;	Conservative 49;	Mismatches 103;	Indels 117;	Gaps 13

```

OY 13 QLCRRGNNSLTTHRRCSPEFLLISSPFCIGLTGMGATQTLRRKSLISSAVATNSLLHDVG 72
OY 61 QIMVFSSSTLTNIQEF-----IISNP-----WLTLAGGIFILLTWIVYMLGEKG--LEKAS 112
OY 73 ATVAIVGAGVALVLPSESLTKENVIQ-----QSLSRKLVHLISGLFLYLAPIFS 122
Db 113 KIMPLIFFLITIVVAQSUTLEGALGVYIIQPRVEDMS-----IQGVLPALGGSFT 166
OY 123 ---GSTEARVPFAVP-----LVNGLRVINGLISPSNMLIKSVTRGRAR 166
Db 167 LSLGTTGMITVASYAPKNNITKSALLSIYVNNIILSVLAGLAFPALKTFGVQPGSG--- 223
OY 167 ELLKGEFLFYVALLLSAVTFRRSPITGMISLMMCGGDGIADIMGKRFSGSTKIPYPRKS 226

```


Db 224 ---FGLLKVLPVSEMTF----- 240
 Qy 227 WAGSIWFIKGFPIISIALYYSSIGYLHMM-----ETTLQVAVMSVAVTESLP 279
 Db 241 --GTFPFYIFLLFLPAL--TSSISLELVNSFTKDNRSKQVAILGISILVPIISIP 296
 Qy 280 IT-----DOLD--DNISVPLATI 295
 Db 297 ATLSFSSLSHLRFAGGTIFDNNDPIVSNILMPLGAL 332

RESULT 6

US-09-134-001C-3935
 ; Sequence 3935, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 3935
 ; LENGTH: 452
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 ; US-09-134-001C-3935

Query Match 6.4%; Score 98.5; DB 2; Length 452;

Best Local Similarity 19.9%; Pred. No. 0.013;
 Matches 67; Conservative 49; Mismatches 103; Indels 117; Gaps 13;

Qy 13 QLCRFNNSLTTHRCSPGFLISPCFGLTGMGSAIQLRARRSLISSAVATNSLHDVG 72
 Db 130 QIMWFKSSTLTNIOFET---IISNP---WLTVLGGGIFILITMVVIMLGVKGS--LEKAS 181
 Qy 73 ATVAVLGGAVYLVLSFESTLTKRNVIQ-----QSLSRKLVIIISGLLFLVAMPIS 122
 Db 182 KIMMPLFLFLITVAQSLTLEGAGVRYLLOPVEWMS-----IGCVLPALGQSFT 235
 Qy 123 ---GSTEARYPAAFV-----LVNGLRLVINGLSISPSMLIKSVTEGRAE 166
 Db 236 LSLGTGMITAYASVPRKMTIKSSALSTIVNMILSVLAGLAIFALKTFFGQPEG--- 292
 Qy 167 ELKGLPLFYVALLESAVFPWRSPDGMISLAMCGGDGIADIMGRKFGSTKIPYPRKS 226
 Db 293 ---GGLLTKVLPVSEMTF----- 309
 Qy 227 WAGSIWFIKGFPIISIALYYSSIGYLHMM-----ETTLQVAVMSVAVTESLP 279
 Db 310 --GTFPFYIFLLFLPAL--TSSISLELVNSFTKDNRSKQVAILGISILVPIISIP 365
 Qy 280 IT-----DOLD--DNISVPLATI 295
 Db 366 ATLSFSSLSHLRFAGGTIFDNNDPIVSNILMPLGAL 401

RESULT 7

US-09-543-681A-4454
 ; Sequence 4454, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRITON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A

; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 4454
 ; LENGTH: 300
 ; TYPE: PRT
 ; ORGANISM: Proteus mirabilis
 ; US-09-543-681A-4454

Query Match

6.3%; Score 97.5; DB 2; Length 300;
 Best Local Similarity 24.9%; Pred. No. 0.0092;
 Matches 66; Conservative 38; Mismatches 78; Indels 83; Gaps 17;

Qy 31 GFLISPCFGLTGMGSAIQLRARRSLISSAVATNSLHDV--GATVAVLGGAVYLVLSF 88
 Db 72 GFLIS-----MIMHG--TPWRARNSFT--RFGHSSLSNEIASGATFFPALGGLWLI--- 118
 Qy 89 ESLTKRNVIQOGLSRKLVIIISGLLFLVLA-----WPIFGSTEARY--PAAFV- 134
 Db 119 SVLAKMPALCKLWLVVMILA-VLFTAIRVYQIDVPTW--YNGITVNFVLTATIG 175
 Qy 135 -PLVNGRLVINGLSISPSMLIKSVTEGRAEILKGLPFYVALLESAVFPWRBS--PI 192
 Db 176 GPILAALIMRIAGFTNLCISAL-----PLLSVIAIITISALVATSGQREL 219
 Qy 193 GMISLAMCGGDGIAD--IMGRKFGSTKI-----PYNPKRSWAGSISMFIFGF 238
 Db 220 GSIOYSQKAVDLPVDVGFMLGILIALTLGLACMIAPLARKNP-----SVSILMVIGF 273
 Qy 239 -----FISIALYYSSIGYLHM 256
 Db 274 ILVVGSEFTGRGVFY-----GLHM 292

RESULT 8

US-09-549-848B-6
 ; Sequence 6, Application US/09549848B
 ; Patent No. 6541259
 ; GENERAL INFORMATION:
 ; APPLICANT: Laessner, Michael
 ; APPLICANT: Post-Bettenmiller, Dusty
 ; APPLICANT: Savidge, Beth
 ; TITLE OF INVENTION: Nucleic Acid Sequences Involved in
 ; TITLE OF INVENTION: Tocopherol Synthesis
 ; FILE REFERENCE: 17133/02/US
 ; CURRENT APPLICATION NUMBER: US/09/549,848B
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/129,899
 ; PRIOR FILING DATE: 1999-04-15
 ; PRIOR APPLICATION NUMBER: 60/146,461
 ; PRIOR FILING DATE: 1999-07-30
 ; NUMBER OF SEQ ID NOS: 94
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 431
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis sp
 ; US-09-549-848B-6

Query Match

6.3%; Score 97; DB 2; Length 431;
 Best Local Similarity 21.9%; Pred. No. 0.019;
 Matches 76; Conservative 50; Mismatches 121; Indels 100; Gaps 18;

Qy 1 MAATLP---LSPINHCRCFNNNSLTTHRCSPGFLISPCFGLTGMGSAIQLRARRS 56
 Db 16 VSSSLPNRRLTPMSRELC-----AVNSFQPFVSTSTAKDITGVRSQANVFATAT 68
 Qy 57 LISSAVATNSLHDVGATVAVLGGAYV-----LVLS 87
 Db 69 AAATATATGTGSSRVALAGLGHVYARCYWELSKAKLSMLVAVTSGTGTYLGTGNAIS 128

Db 256 IVPBMRGADPKPRKATVGMALTTTLALVPLSVISLNGLDJNDVATISMGRLG 315

Cy 216 STKIPNPKSMAGS 230

Db 316 -----EMASS 320

RESULT 12

US-08-672-814D-2

Sequence 2, Application US/08672814D

Patent No. 5952480

GENERAL INFORMATION:

APPLICANT: Leung, David W.

TITLE OF INVENTION: MAMMALIAN

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Cell Therapeutics, Inc.

STREET: 201 Elliott Avenue West

CITY: Seattle

STATE: Washington

COUNTRY: U.S.A.

ZIP: 98119

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" disk, 1.44Mb, double side, high density

COMPUTER: PC Clone (486 microprocessor)

OPERATING SYSTEM: MS-DOS Version 6.1, Windows NT

SOFTWARE: WORD 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,814D

FILING DATE: 28-Jun-1996

ATTORNEY/AGENT INFORMATION:

NAME: Faciszewski, Stephen

REGISTRATION NUMBER: 36,131

REFERENCE/DOCKET NUMBER: 1803

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)282-7100

TELEFAX: (206)284-6206

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 461

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: polypeptide

HYPOTHETICAL: no

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM: homo sapien

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE:

ORGANELLE:

FEATURE:

NAME/KEY: CDS

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

US-08-672-814D-2

Query Match 6.2%; Score 95; DB 1; Length 461;

Best Local Similarity 26.9%; Pred. No. 0.036; Mismatches 54; Indels 40; Gaps 8;

Matches 42; Conservative 20; Mismatches 54; Indels 40; Gaps 8;

Cy 121 FSGSTEARYPAPAPF-----LVNGGLVINGLSISPSNLSIKSVTEGRABEILKGPL 173

Db 157 FYGGETVADYFATFQREBQQLIRYHRFISFALYLAFCMFVLSVVENHRLQ----- 210

Cy 174 FYVLA-----LFSAVF---FYRESPIGMSIAMCGDGIADIMGRKGS 216

Db 211 FYMFAMTHVTLITVTQSHLVQNLFGMTFVLPIS---SVIC-NDITAYLFGFFGR 265

Cy 217 TK-IPYNPKSMAGSISMF-----IFGFISIALLY 247

Db 266 TPLIKSPKTKWEGFISGFSTVVFGLIAVVLKY 301

RESULT 13

US-09-333-696-2

Sequence 2, Application US/09333696

Patent No. 6200769

GENERAL INFORMATION:

APPLICANT: Leung, David W.

TITLE OF INVENTION: MAMMALIAN

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Cell Therapeutics, Inc.

STREET: 201 Elliott Avenue West

CITY: Seattle

STATE: Washington

COUNTRY: U.S.A.

ZIP: 98119

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" disk, 1.44Mb, double side, high density

COMPUTER: PC Clone (486 microprocessor)

OPERATING SYSTEM: MS-DOS Version 6.1, Windows NT

SOFTWARE: WORD 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/333,696

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/672,814

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Faciszewski, Stephen

REGISTRATION NUMBER: 36,131

REFERENCE/DOCKET NUMBER: 1803

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)282-7100

TELEFAX: (206)284-6206

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 461

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: polypeptide

HYPOTHETICAL: no

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM: homo sapien

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE:

ORGANELLE:

FEATURE:

NAME/KEY: CDS

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

US-09-333-696-2

Query Match 6.2%; Score 95; DB 2; Length 461;

Best Local Similarity 26.9%; Pred. No. 0.036;

Matches 42; Conservative 20; Mismatches 54; Indels 40; Gaps 8;
QY 121 FSGSTEARYPAFP-----LYNGLRLVINGLSISPSMLIKSVREGRAEELKGPL 173
DB 157 FYGETVADYFATFVOREBQLOFLIRYHRFISFALYAGFCMFVLSVKEHYRLQ----- 210
QY 174 FYVLA-----LFSAVF---FWRESPIGMSIAMMCGGDGIADIMGRKFGS 216
DB 211 FYMAFWHTVTLITVYQSHLVIONLFEGMIWFLVPIS---SVLC-NDITAYLGFPPFGR 265
QY 217 TK-IPYPRKSWAGSISMF---IFGFISIALLY 247
DB 266 TPLIKLSPKKTWEGFISGFSTVVGFIYAAYLSKY 301
RESULT 14
US-09-282-218A-2
; Sequence 2, Application US/09282218A
; Patent No. 6503700
; GENERAL INFORMATION:
; APPLICANT: LEUNG, David W.
; TITLE OF INVENTION: MAMMALIAN CDP-DIACYLGLYCEROL SYNTHASE
; FILE REFERENCE: 077319/0153
; CURRENT APPLICATION NUMBER: US/09/282,218A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 2
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-282-218A-2

Query Match 6.2%; Score 95; DB 2; Length 461;
Best Local Similarity 26.9%; Pred. No. 0.036;
Matches 42; Conservative 20; Mismatches 54; Indels 40; Gaps 8;
QY 121 FSGSTEARYPAFP-----LYNGLRLVINGLSISPSMLIKSVREGRAEELKGPL 173
DB 157 FYGETVADYFATFVOREBQLOFLIRYHRFISFALYAGFCMFVLSVKEHYRLQ----- 210
QY 174 FYVLA-----LFSAVF---FWRESPIGMSIAMMCGGDGIADIMGRKFGS 216
DB 211 FYMAFWHTVTLITVYQSHLVIONLFEGMIWFLVPIS---SVLC-NDITAYLGFPPFGR 265
QY 217 TK-IPYPRKSWAGSISMF---IFGFISIALLY 247
DB 266 TPLIKLSPKKTWEGFISGFSTVVGFIYAAYLSKY 301

RESULT 15
US-09-134-001C-5009
; Sequence 5009, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5009
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5009

Query Match 6.2%; Score 94.5; DB 2; Length 424;

Best Local Similarity 20.8%; Pred. No. 0.036;
Matches 66; Conservative 55; Mismatches 108; Indels 89; Gaps 16;
QY 10 INHOLCFGNNSL-----TTHRCSP--GFLISSPCFGLGTWGSATOLARSLISSA 61
DB 10 VQHLAMTAGAILPPIIVGTSLSKFSABEIALYLVDFM-----CGVATFLQANK----- 59
QY 62 VATNSLHDVCAATVAVGAYAVLV--SFESLTRNVIQOSLSRKYH---ILSGLLFVL 116
DB 60 -----VGTGLPIVLGCTFTAVAMMILIGQTKGLDVLVYSGLLSGLVLV 104
QY 117 AMPIFSGSTEARYPAFV-PLVNGRLVINGLSISPSMLI---KSVTREGRAEELKGL 171
DB 105 IAPFFS-----YVKEFPFPVVTGSVVTIIGINIMPVAMNYIAGEGAKXNGDTKNLILG 158
QY 172 PLFYVALL--FSAVFWRRESPIGMSIAMMCG---GDGIADIMGRKFGSTKI-PYNDRK 225
DB 159 GVTLLIILILQRFYKGF-----LKSIALILGLAIGTALAGI---FGNVDIKQVGDA 206
QY 226 SWAGSISMF---FGFISIALLY-----YSSLGILHNNWETTLQRV----- 265
DB 207 HMRGFPVPRFSGRGFDVSSILVFIVAVVSLISTGVYHALSEITGRKLERKOPRKGYT 266
QY 266 --ANVSNAATVESLPIT 281
DB 267 AEGLAIIIGSIFNAPPYT 284

Search completed: March 16, 2006, 19:52:02
Job time : 30 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 16, 2006, 19:51:40 ; Search time 79 Seconds
(without alignments)
1607.850 Million cell updates/sec

Title: US-10-634-548-2

Perfect score: 1536
Sequence: 1 MAATLPLSPINHQCRCFGNN.....DNISVPLATILAAVLSFGY 304

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA Main:

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1536	100.0	304	US-10-634-548-2	Sequence 2, Appl1
2	1536	100.0	315	US-10-425-114-54545	Sequence 54545, A
3	1523	99.2	301	US-10-425-114-54546	Sequence 54546, A
4	1266	82.4	304	US-10-634-548-39	Sequence 39, Appl1
5	1266	82.4	319	US-10-425-114-54630	Sequence 54630, A
6	1140	74.2	226	US-10-634-548-4	Sequence 4, Appl1
7	870	56.6	306	US-10-425-114-54635	Sequence 54635, A
8	864	56.2	298	US-10-634-548-41	Sequence 41, Appl1
9	857.5	55.8	302	US-10-634-548-45	Sequence 45, Appl1
10	791.5	51.5	314	US-10-634-548-46	Sequence 46, Appl1
11	791.5	51.5	332	US-10-425-114-55785	Sequence 55785, A
12	791.5	51.5	657	US-10-634-548-49	Sequence 49, Appl1
13	791.5	51.5	657	US-10-437-963-179783	Sequence 179783, A
14	791.5	51.5	803	US-10-634-548-48	Sequence 48, Appl1
15	791.5	51.5	803	US-10-437-963-179784	Sequence 179784, A
16	786	51.2	309	US-10-425-114-55436	Sequence 55436, A
17	782.5	50.9	269	US-10-634-548-47	Sequence 47, Appl1
18	777	50.6	303	US-10-634-548-61	Sequence 61, Appl1
19	776	50.5	251	US-10-425-114-55867	Sequence 55867, A
20	776	50.5	268	US-10-425-115-303416	Sequence 303416, A
21	773	50.3	300	US-10-634-548-58	Sequence 58, Appl1
22	773	50.3	312	US-10-425-114-54641	Sequence 54641, A
23	752.5	49.0	267	US-10-634-548-62	Sequence 62, Appl1
24	751	48.9	233	US-10-425-114-54631	Sequence 54631, A
25	751	48.9	236	US-10-425-114-55714	Sequence 55714, A
26	751	48.9	236	US-10-634-548-63	Sequence 63, Appl1
27	718.5	46.8	292	US-10-634-548-44	Sequence 44, Appl1

28	646	42.1	199	US-10-425-114-72714	Sequence 72714, A
29	615	40.0	191	US-10-634-548-55	Sequence 55, Appl1
30	615	40.0	191	US-10-767-701-42774	Sequence 42774, A
31	607	39.5	259	US-10-739-930-8545	Sequence 8545, Ap
32	604	39.3	265	US-10-424-599-255091	Sequence 255091, A
33	591	38.5	188	US-10-634-548-60	Sequence 60, Appl1
34	583	38.0	211	US-10-425-115-103417	Sequence 303417, A
35	580.5	37.8	292	US-10-767-701-43330	Sequence 43330, A
36	572.5	37.3	312	US-10-634-548-65	Sequence 65, Appl1
37	572.5	37.3	313	US-10-425-115-357166	Sequence 357166, A
38	572.5	37.3	338	US-10-425-114-55756	Sequence 55756, A
39	565.5	36.8	246	US-10-634-548-50	Sequence 50, Appl1
40	562.5	36.6	302	US-10-634-548-54	Sequence 64, Appl1
41	552.5	36.0	296	US-10-425-114-54640	Sequence 54640, A
42	552.5	36.0	296	US-10-634-548-56	Sequence 56, Appl1
43	544	35.4	346	US-10-739-930-10410	Sequence 10410, A
44	543.5	35.4	319	US-10-424-599-213867	Sequence 213867, A
45	542.5	35.3	319	US-10-634-548-43	Sequence 43, Appl1

ALIGNMENTS

RESULT 1

US-10-634-548-2 Application US/10634548

Publication No. US20040045051A1

GENERAL INFORMATION:

APPLICANT: No. US20040045051A1r1s, Susan R

APPLICANT: Lincoln, Kim

APPLICANT: Abad, Mark Scott

APPLICANT: Eilers, Robert

APPLICANT: Hartsuyker, Karen Kindle

APPLICANT: Hirschberg, Joseph

APPLICANT: Karunanandaa, Balasulojini

APPLICANT: Moshiri, Farhad

APPLICANT: Stein, Joshua C.

APPLICANT: Valentin, Henry B.

APPLICANT: Venkatesh, Tyamagondlu V.

TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof

FILE REFERENCE: Ren-01-125

CURRENT APPLICATION NUMBER: US/10/634,548

CURRENT FILING DATE: 2003-08-05

PRIOR APPLICATION NUMBER: us 60/400,689

PRIOR FILING DATE: 2002-08-05

NUMBER OF SEQ ID NOS: 79

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2

LENGTH: 304

TYPE: PRT

ORGANISM: Arabidopsis thaliana

US-10-634-548-2

Query Match

Best Local Similarity 100.0%; Pred. No. 1, 1e-151; Length 304;

Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAATLPLSPINHQCRCFGNNSTTHRCSPGFLISSPCFGLTGMGATQARARSLISS	60
DB	1	MAATLPLSPINHQCRCFGNNSTTHRCSPGFLISSPCFGLTGMGATQARARSLISS	60
QY	61	AAATNSLHDVGAAVAVLGAVALVLSFESTTKRNVOQSLSRGLVHLSGLFVLAMPI	120
DB	61	AAATNSLHDVGAAVAVLGAVALVLSFESTTKRNVOQSLSRGLVHLSGLFVLAMPI	120
QY	121	FSGSTEARFPAFVPLVNGRLVINGSLSPNSMLIKSVTRGAEELKGPLFYVALL	180
DB	121	FSGSTEARFPAFVPLVNGRLVINGSLSPNSMLIKSVTRGAEELKGPLFYVALL	180
QY	181	FSFAVFPRESPIGMSIAMMGCGDGIADIMGRKFGSTKIPYNPXKSWAGSISMTFGPFI	240
DB	181	FSFAVFPRESPIGMSIAMMGCGDGIADIMGRKFGSTKIPYNPXKSWAGSISMTFGPFI	240

OY 241 STALLYYSSLGYLHMMWETTLQRYAVMSVATVVESSLPITDQDDNISVPLATILAAVL 300
 |||||
 Db 241 STALLYYSSLGYLHMMWETTLQRYAVMSVATVVESSLPITDQDDNISVPLATILAAVL 300
 |||||
 OY 301 SFGY 304
 |||||
 Db 301 SFGY 304

RESULT 2

US-10-425-114-54545
 ; Sequence 54545, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingtong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 54545
 ; LENGTH: 315
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana columbia
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3278-077-D5_FLI.pep
 US-10-425-114-54545

Query Match 100.0%; Score 1536; DB 4; Length 315;
 Best Local Similarity 100.0%; Pred. No. 1,2e-151;
 Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAATPLSPINHOICRFNNNSLTTHRFCSPGFLISSPCFGLTGMGSATOLRARRSLISS 60
 |||||
 Db 12 MAATPLSPINHOICRFNNNSLTTHRFCSPGFLISSPCFGLTGMGSATOLRARRSLISS 71
 |||||
 OY 61 AVATNSLHDVGATVAVLGAVALVLSFESLTKRNVIOQSLSRKLVHILSGLLFVLAMP 120
 |||||
 Db 72 AVATNSLHDVGATVAVLGAVALVLSFESLTKRNVIOQSLSRKLVHILSGLLFVLAMP 131
 |||||
 OY 121 FSGSTEARYFAAFVPLVNGRLVINGLSISPSNMLIKSVTRBGRABELKGPLFYVAL 180
 |||||
 Db 132 FSGSTEARYFAAFVPLVNGRLVINGLSISPSNMLIKSVTRBGRABELKGPLFYVAL 191
 |||||
 OY 181 FSAVFEMRESPTIGMTSLMMCGDGIADIMGRKPGSTKIPYPRKSWAGSISMFIFGFEI 240
 |||||
 Db 192 FSAVFEMRESPTIGMTSLMMCGDGIADIMGRKPGSTKIPYPRKSWAGSISMFIFGFEI 251
 |||||
 OY 241 STALLYYSSLGYLHMMWETTLQRYAVMSVATVVESSLPITDQDDNISVPLATILAAVL 300
 |||||
 Db 252 STALLYYSSLGYLHMMWETTLQRYAVMSVATVVESSLPITDQDDNISVPLATILAAVL 311
 |||||
 OY 301 SFGY 304
 |||||
 Db 312 SFGY 315

RESULT 3

US-10-425-114-54546
 ; Sequence 54546, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingtong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 54546
 ; LENGTH: 301
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB23-048-A2_FLI.pep
 US-10-425-114-54546

Query Match 99.2%; Score 1523; DB 4; Length 301;
 Best Local Similarity 100.0%; Pred. No. 2.6e-150;
 Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TLPLSPINHOICRFNNNSLTTHRFCSPGFLISSPCFGLTGMGSATOLRARRSLISSAVA 63
 |||||
 Db 1 TLPLSPINHOICRFNNNSLTTHRFCSPGFLISSPCFGLTGMGSATOLRARRSLISSAVA 60
 |||||
 OY 64 TNSLHDVGATVAVLGAVALVLSFESLTKRNVIOQSLSRKLVHILSGLLFVLAMPFSG 123
 |||||
 Db 61 TNSLHDVGATVAVLGAVALVLSFESLTKRNVIOQSLSRKLVHILSGLLFVLAMPFSG 120
 |||||
 OY 124 STEARYFAAFVPLVNGRLVINGLSISPSNMLIKSVTRBGRABELKGPLFYVALFSA 183
 |||||
 Db 121 STEARYFAAFVPLVNGRLVINGLSISPSNMLIKSVTRBGRABELKGPLFYVALFSA 180
 |||||
 OY 184 VFVRESPTIGMTSLMMCGDGIADIMGRKPGSTKIPYPRKSWAGSISMFIFGFEISIA 243
 |||||
 Db 181 VFVRESPTIGMTSLMMCGDGIADIMGRKPGSTKIPYPRKSWAGSISMFIFGFEISIA 240
 |||||
 OY 244 LLYYSSLGYLHMMWETTLQRYAVMSVATVVESSLPITDQDDNISVPLATILAAVLSFG 303
 |||||
 Db 241 LLYYSSLGYLHMMWETTLQRYAVMSVATVVESSLPITDQDDNISVPLATILAAVLSFG 300
 |||||
 OY 304 Y 304
 |||||
 Db 301 Y 301

RESULT 4

US-10-634-548-39
 ; Sequence 39, Application US/10634548
 ; Publication No. US20040045051A1
 ; GENERAL INFORMATION:
 ; APPLICANT: No. US20040045051A1ris, Susan R
 ; APPLICANT: Lincoln, Kim
 ; APPLICANT: Abad, Mark Scott
 ; APPLICANT: Eilers, Robert
 ; APPLICANT: Hartsuiker, Karen Kindle
 ; APPLICANT: Hirschberg, Joseph
 ; APPLICANT: Karunanandaa, Balasubramanian
 ; APPLICANT: Moshiri, Farhad
 ; APPLICANT: Stein, Joshua C.
 ; APPLICANT: Valentin, Henry E.
 ; APPLICANT: Venkatesh, Tyamagondlu V.
 ; TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof
 ; FILE REFERENCE: Ren-01-125
 ; CURRENT APPLICATION NUMBER: US/10/634,548
 ; CURRENT FILING DATE: 2003-08-05
 ; PRIOR APPLICATION NUMBER: us 60/400,689
 ; NUMBER OF SEQ ID NOS: 79
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 39
 ; LENGTH: 304
 ; TYPE: PRT
 ; ORGANISM: Brassica napus
 US-10-634-548-39

Query Match 82.4%; Score 1266; DB 4; Length 304;
 Best Local Similarity 81.4%; Pred. No. 1.9e-123;
 Matches 250; Conservative 24; Mismatches 27; Indels 6; Gaps 2;

QY 1 MAATLPLSPINHQCRCFGNN--SLTTHRFCSPGFLISSPCFISGLTGMGSAATOLRARRSL 57
 DB 1 MAALPLSPVSHQCRCISNRFWYNAAMTRPCSP---VSSPCYIGVKIGSSSQARARHPL 57
 QY 58 ISSAVATNSLHDVGAATVAVLGAVYALVLSFESLTKRNVIQOQSLSRKLVHILSGLLFVLA 117
 DB 58 ISSASTDYLDHVGATVAVLGAVYALVLSFESLTKRDVIRQRLSRKLVHILSGLLFALS 117
 QY 118 WPTSGSTEARYPFAFVPLVNGRLVINGLSISPSNMLIKSVTEGRAEELKGPLFYVLA 177
 DB 118 WPTSGSTEARYPFAFVPLVNGRLVINGLSISPSNMLIKSVTEGRAEELKGPLFYVLA 177
 QY 178 ALFSAVFFWRSDPTGMISLAMCGGDIADIMGRKFGSTKIPYNPRKSLAGSISMFTFG 237
 DB 178 ALFVAVFFWRSDPTGMISLAMCGGDIADIMGRKGSYKIPYNPRKSLAGSISMFTFG 237
 QY 238 PFISIGLYYSSSLGYLHMWETTLQRYAMVSMVATVESLPTDQDDNISVPLATILA 297
 DB 238 PFISIGLYYSSSLGYLHMWETTLQRYAMVSMVATVESLPTDQDDNISVPLATILA 297
 QY 298 AYLSFGY 304
 DB 298 AYLSFGY 304

RESULT 5

US-10-425-114-54630
 ; Sequence 54630, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 54630
 ; LENGTH: 319
 ; TYPE: PRT
 ; ORGANISM: Brassica napus
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB82-020-B9_FIL_PEP
 ; US-10-425-114-54630

Query Match 82.4%; Score 1266; DB 4; Length 319;
 Best Local Similarity 81.4%; Pred. No. 2.1e-123;
 Matches 250; Conservative 24; Mismatches 27; Indels 6; Gaps 2;

QY 1 MAATLPLSPINHQCRCFGNN--SLTTHRFCSPGFLISSPCFISGLTGMGSAATOLRARRSL 57
 DB 16 MAALPLSPVSHQCRCISNRFWYNAAMTRPCSP---VSSPCYIGVKIGSSSQARARHPL 72
 QY 58 ISSAVATNSLHDVGAATVAVLGAVYALVLSFESLTKRNVIQOQSLSRKLVHILSGLLFVLA 117
 DB 73 ISSASTDYLDHVGATVAVLGAVYALVLSFESLTKRDVIRQRLSRKLVHILSGLLFALS 132
 QY 118 WPTSGSTEARYPFAFVPLVNGRLVINGLSISPSNMLIKSVTEGRAEELKGPLFYVLA 177
 DB 133 WPTSGSTEARYPFAFVPLVNGRLVINGLSISPSNMLIKSVTEGRAEELKGPLFYVLA 192
 QY 178 ALFSAVFFWRSDPTGMISLAMCGGDIADIMGRKFGSTKIPYNPRKSLAGSISMFTFG 237
 DB 178 ALFSAVFFWRSDPTGMISLAMCGGDIADIMGRKFGSTKIPYNPRKSLAGSISMFTFG 237

DB 193 ALFVAVFFWRSDPTGMISLAMCGGDIADIMGRKGSYKIPYNPRKSLAGSISMFTFG 252
 QY 238 PFISIGLYYSSSLGYLHMWETTLQRYAMVSMVATVESLPTDQDDNISVPLATILA 297
 DB 253 PFISIGLYYSSSLGYLHMWETTLQRYAMVSMVATVESLPTDQDDNISVPLATILA 312
 QY 298 AYLSFGY 304
 DB 313 AYLSFGY 319

RESULT 6

US-10-634-548-4
 ; Sequence 4, Application US/10634548
 ; Publication No. US20040045051A1
 ; GENERAL INFORMATION:
 ; APPLICANT: No. US20040045051A1's, Susan R
 ; APPLICANT: Lincoln, Kim
 ; APPLICANT: Abad, Mark Scott
 ; APPLICANT: Elfers, Robert
 ; APPLICANT: Hartsuyker, Karen Kindle
 ; APPLICANT: Hirschberg, Joseph
 ; APPLICANT: Karunanandaa, Balasubramanian
 ; APPLICANT: Moshiri, Farhad
 ; APPLICANT: Stein, Joshua C.
 ; APPLICANT: Valentin, Henry E.
 ; APPLICANT: Venkatesh, Tyamagondlu V.
 ; TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof
 ; FILE REFERENCE: Ren-01-125
 ; CURRENT APPLICATION NUMBER: US/10/634,548
 ; CURRENT FILING DATE: 2003-08-05
 ; PRIOR APPLICATION NUMBER: us 60/400,689
 ; PRIOR FILING DATE: 2002-08-05
 ; NUMBER OF SEQ ID NOS: 79
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 4
 ; LENGTH: 226
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-634-548-4

Query Match 74.2%; Score 1140; DB 4; Length 226;
 Best Local Similarity 100.0%; Pred. No. 1.9e-110;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAATLPLSPINHQCRCFGNN--SLTTHRFCSPGFLISSPCFISGLTGMGSAATOLRARRSL 60
 DB 1 MAATLPLSPINHQCRCFGNN--SLTTHRFCSPGFLISSPCFISGLTGMGSAATOLRARRSL 60
 QY 61 AVATNSLHDVGAATVAVLGAVYALVLSFESLTKRNVIQOQSLSRKLVHILSGLLFVLA 120
 DB 61 AVATNSLHDVGAATVAVLGAVYALVLSFESLTKRNVIQOQSLSRKLVHILSGLLFVLA 120
 QY 121 FSGSTEARYPFAFVPLVNGRLVINGLSISPSNMLIKSVTEGRAEELKGPLFYVLA 180
 DB 121 FSGSTEARYPFAFVPLVNGRLVINGLSISPSNMLIKSVTEGRAEELKGPLFYVLA 180
 QY 181 FSAVFFWRSDPTGMISLAMCGGDIADIMGRKFGSTKIPYNPRKS 226
 DB 181 FSAVFFWRSDPTGMISLAMCGGDIADIMGRKFGSTKIPYNPRKS 226

RESULT 7

US-10-425-114-54635
 ; Sequence 54635, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-22(5313)B
 CURRENT APPLICATION NUMBER: US/10/425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 54635
 LENGTH: 306
 TYPE: PRT
 ORGANISM: Gossypium hirsutum
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB3196-048-All_Flt.pep
 US-10-425-114-54635

Query Match 56.6%; Score 870; DB 4; Length 306;
 Best Local Similarity 56.7%; Pred. No. 4.9e-82;
 Matches 174; Conservative 51; Mismatches 72; Indels 10; Gaps 2;

QY 2 AATPLSPINHQCFGNNSLTTRFCS----PGFLISSPCFGLTGMSATOLARRSL 57
 DB 6 AATMSLS-----LSFTPIILSRHYSAVFPFPRFLFSLPIPTSRPILYRAPQRATA 59
 QY 58 ISSAVATNSLHDVATVAVLGGAYATVLSFESLTGRNVIOQSLSRKLVHLSGLFTLA 117
 DB 60 LSATVATSIERDTRMASAVFAGAYALVFTFDILTOKELIQONLSRKLVHLSGLFAIS 119
 QY 118 WPIESGSTEARYFAFVPLVNGLRVINGLSISPSNMLIKSVTRGRABELLKGPLFYVL 177
 DB 120 WPIFNADBARFASVLPFLNCLRVHLSLTDOSLIKSVTRGRNPKELRGPLYVA 179
 QY 178 ALFSAVFWRBSPIGMISLAMCGDGIADIIMGRKFGSTKIPYNPBKSWAGSISMPIFG 237
 DB 180 MMLCALVWRBSPVGVCLAMCGDGVADIIGKYSKIPYNOGSWAGSISMPIFG 239
 QY 238 FFISIALIYYSSLSGLYHNMETTYQRYAMVSMVATVYESLPITDLDNISVPLATILA 297
 DB 240 FIIISGMYYSALGYLIDMGYTLHRAVATSLVATVYESLPISMLIDNISVPLASMLA 299
 QY 298 AYLISFGY 304
 DB 300 AYLTPGH 306

RESULT 8

US-10-634-548-41
 Sequence 41, Application US/10634548
 Publication No. US20040045051A1

GENERAL INFORMATION:

APPLICANT: No. US20040045051A1rIs, Susan R

APPLICANT: Lincoln, Kim

APPLICANT: Abad, Mark Scott

APPLICANT: Eilers, Robert

APPLICANT: Hartsuyker, Karen Kindle

APPLICANT: Hirschberg, Joseph

APPLICANT: Karunanandaa, Balasulojini

APPLICANT: Moshiri, Farhad

APPLICANT: Stein, Joshua C.

APPLICANT: Valentin, Henry E.

APPLICANT: Venkatesh, Tyamagondlu V.

TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof

FILE REFERENCE: Ren-01-125

CURRENT APPLICATION NUMBER: US/10/634,548

PRIOR FILING DATE: 2003-08-05

PRIOR APPLICATION NUMBER: us 60/400,689

NUMBER OF SEQ ID NOS: 79

SOFTWARE: PatentIn version 3.2

SEQ ID NO 41

LENGTH: 298

TYPE: PRT

ORGANISM: Gossypium hirsutum

US-10-634-548-41

Query Match 56.2%; Score 864; DB 4; Length 298;
 Best Local Similarity 60.1%; Pred. No. 2e-81;
 Matches 167; Conservative 46; Mismatches 65; Indels 0; Gaps 0;

QY 27 FCGSPFLISSPCFGLTGMSATOLARRSLISSAVATNSLHDVATVAVLGGAYATVL 86
 DB 21 FPPPRFLFSLPILPTTSRFPILYRAPQRATVAATVATASIFRTAASASVFAAYALVF 80
 QY 87 SFESLTGRNVIOQSLSRKLVHLSGLFLVLAIPFSGSTEARYFAFVPLVNGLRVING 146
 DB 81 TFDILTQKELIQONLSRKLVHLSGLFLASWPIFSNADBARFASVLPFLNCLRVYHG 140
 QY 147 LSISPSNMLIKSVTRGRABELLKGPLFYVALIFSAVFWRESPIGMISLAMCGDGI 206
 DB 141 LSLTDDQSLIKSVTRBGNPKELRGPLYVAMLMCALVWRBSPGVICLAMCGDGV 200
 QY 207 ADIMGRKFGSTKIPYNPBKSWAGSISMPIFGFISIALIYYSSLSGLYHNMETTYQRYA 266
 DB 201 ADIIGRKYGSKIPYNOGSWAGSISMPIFGFIIISIMLYYSALGYLIDMGYTLHRA 260
 QY 267 MVMWATVYESLPITDLDNISVPLATILAAYLISFGY 304
 DB 261 FISLVATVYESLPISMLIDNISVPLASMLAAYLTPGH 298

RESULT 9

US-10-634-548-45

Sequence 45, Application US/10634548

Publication No. US20040045051A1

GENERAL INFORMATION:

APPLICANT: No. US20040045051A1rIs, Susan R

APPLICANT: Lincoln, Kim

APPLICANT: Abad, Mark Scott

APPLICANT: Eilers, Robert

APPLICANT: Hartsuyker, Karen Kindle

APPLICANT: Hirschberg, Joseph

APPLICANT: Karunanandaa, Balasulojini

APPLICANT: Moshiri, Farhad

APPLICANT: Stein, Joshua C.

APPLICANT: Valentin, Henry E.

APPLICANT: Venkatesh, Tyamagondlu V.

TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof

FILE REFERENCE: Ren-01-125

CURRENT APPLICATION NUMBER: US/10/634,548

PRIOR FILING DATE: 2003-08-05

PRIOR APPLICATION NUMBER: us 60/400,689

NUMBER OF SEQ ID NOS: 79

SOFTWARE: PatentIn version 3.2

SEQ ID NO 45

LENGTH: 302

TYPE: PRT

ORGANISM: Glycine max

US-10-634-548-45

Query Match 55.8%; Score 857.5; DB 4; Length 302;
 Best Local Similarity 60.6%; Pred. No. 9.8e-81;
 Matches 175; Conservative 44; Mismatches 51; Indels 19; Gaps 5;

QY 19 NNSLTTH--RF--CGSPFLISSPCFGLTGMSATOL--RARRSLISSAVATNSLHDVGA 73
 DB 26 NSPTNTHVRLCSP-----GVPPAVRLDQRLRFPVPPGGA--EDLLYNAGA 71
 QY 74 TVAVTGAAYATVLSFESLTGRNVIOQSLSRKLVHLSGLFLVLAIPFSGSTEARYFAF 133
 DB 72 TVGVAGGVAVRPADELTRRNVIQOGLSRKLVHLSGLFLVSWPIFSNPKARYFAAF 131
 QY 134 VPLVNGLRVINGLSISPSNMLIKSVTRGRABELLKGPLFYVALIFSAVFWRESPIG 193
 DB 132 VPLVNGLRVINGLSISPSNMLIKSVTRBGNPKELRGPLYVAMLMCALVWRBSPGVIC 191
 QY 194 MISLAMCGDGIADIMGRKFGSTKIPYNPBKSWAGSISMPIFGFISIALIYYSSLSGY 253

Db 192 VISLMMCGADGDIADIGRRYGMKIPYNEHKSLSGMSMLVFGFVLSIGMLYYYSVLGH 251
Qy 254 LHMWETTLQKVAVMSWATVYESPIPDQDDNISVPLATITLAAYLSF 302
Db 252 VOLDMASTLPRVAFISFVATLVESLPITKVVDDNISVPLATMAVAAPFTF 300

RESULT 10
US-10-634-548-46
Sequence 46, Application US/10634548
Publication No. US20040045051A1
GENERAL INFORMATION:
APPLICANT: No. US20040045051A1ris, Susan R
APPLICANT: Lincoln, Kim
APPLICANT: Abad, Mark Scott
APPLICANT: Elstner, Robert
APPLICANT: Hartsuiker, Karen Kindle
APPLICANT: Hirschberg, Joseph
APPLICANT: Karunanandaa, Balasubramanian
APPLICANT: Moehrl, Farhad
APPLICANT: Stein, Joshua C.
APPLICANT: Valentini, Henry E.
APPLICANT: Venkatesh, Tyamagondlu V.
TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof
FILE REFERENCE: Ren-01-125
CURRENT APPLICATION NUMBER: US/10/634,548
PRIORITY FILING DATE: 2003-08-05
PRIORITY FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.2
SEQ ID NO 46
LENGTH: 314
TYPE: PRT
ORGANISM: Oryza sativa
US-10-634-548-46

Query Match 51.5%; Score 791.5; DB 4; Length 314;
Best Local Similarity 51.1%; Pred. No. 8.2e-74;
Matches 159; Conservative 60; Mismatches 81; Indels 11; Gaps 4;

Qy 2 AATPLSPINHQCR---FGNNSL-----TTRFCSPGFLISSPCFIGHT-GMGSATQORA 53
Db 3 AAAPVDVVRHFPCCSSVVAASSLSRSKSLASPAASASRRRLVGVGAAA---A 59
Qy 54 RRLSSAVATNSLHVDGATVAVLGGAYALVLSFESITKXNVIOQSISRLVHTLSGL 113
Db 60 PAVAAALASATPALRDCATLITAGAYSLVRAFDGLTARLLEQNSRKIVHVLSCVL 119
Qy 114 FVLAMPFSGSTEARFPAFVPLVNGRLVINGLSISNSMLISVREGRAEELKGPL 173
Db 120 FMSSWPLFSNSTEARFPAFVPLVNCRLTYGLRLSTDELAVSVREGREBELKGPL 179
Qy 174 FVVALALFSAVFFWRRESPIGMISLMMCGDGIADIMGRKFGSTKIPNPKRSWAGSISM 233
Db 180 YVIVLVLSVLFVRQSPIGIVSLMSMGSGDPADIVGRYGSAPKLPENKSKWIGSISM 239
Qy 234 FIFGFFISIALIYYSSIGYLMHWETTLQKVAVMSWATVYESLPITDQDDNISVPLA 293
Db 240 FIFGFFLSALMLFFSCIGYFTVCMDLALGKLALVALAATVEECIPVNDVDDNISVPLA 299
Qy 294 TILAAYLSFGY 304
Db 300 TMLAAYLLFGY 310

RESULT 11
US-10-425-114-55785
Sequence 55785, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdeng
APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
PRIORITY FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 55785
LENGTH: 332
TYPE: PRT
ORGANISM: Oryza sativa nipponbare
FEATURE:
OTHER INFORMATION: Clone ID: LIB3432-014-E9_FLI.pep
US-10-425-114-55785

Query Match 51.5%; Score 791.5; DB 4; Length 332;
Best Local Similarity 51.1%; Pred. No. 8.9e-74;
Matches 159; Conservative 60; Mismatches 81; Indels 11; Gaps 4;

Qy 2 AATPLSPINHQCR---FGNNSL-----TTRFCSPGFLISSPCFIGHT-GMGSATQORA 53
Db 21 AAAPVDVVRHFPCCSSVVAASSLSRSKSLASPAASASRRRLVGVGAAA---A 77
Qy 54 RRLSSAVATNSLHVDGATVAVLGGAYALVLSFESITKXNVIOQSISRLVHTLSGL 113
Db 78 PAVAAALASATPALRDCATLITAGAYSLVRAFDGLTARLLEQNSRKIVHVLSCVL 137
Qy 114 FVLAMPFSGSTEARFPAFVPLVNGRLVINGLSISNSMLISVREGRAEELKGPL 173
Db 138 FMSSWPLFSNSTEARFPAFVPLVNCRLTYGLRLSTDELAVSVREGREBELKGPL 197
Qy 174 FVVALALFSAVFFWRRESPIGMISLMMCGDGIADIMGRKFGSTKIPNPKRSWAGSISM 233
Db 198 YVIVLVLSVLFVRQSPIGIVSLMSMGSGDPADIVGRYGSAPKLPENKSKWIGSISM 257
Qy 234 FIFGFFISIALIYYSSIGYLMHWETTLQKVAVMSWATVYESLPITDQDDNISVPLA 293
Db 258 FIFGFFLSALMLFFSCIGYFTVCMDLALGKLALVALAATVEECIPVNDVDDNISVPLA 317
Qy 294 TILAAYLSFGY 304
Db 318 TMLAAYLLFGY 328

RESULT 12
US-10-634-548-49
Sequence 49, Application US/10634548
Publication No. US20040045051A1
GENERAL INFORMATION:
APPLICANT: No. US20040045051A1ris, Susan R
APPLICANT: Lincoln, Kim
APPLICANT: Abad, Mark Scott
APPLICANT: Elstner, Robert
APPLICANT: Hartsuiker, Karen Kindle
APPLICANT: Hirschberg, Joseph
APPLICANT: Karunanandaa, Balasubramanian
APPLICANT: Moehrl, Farhad
APPLICANT: Stein, Joshua C.
APPLICANT: Valentini, Henry E.
APPLICANT: Venkatesh, Tyamagondlu V.
TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof
FILE REFERENCE: Ren-01-125
CURRENT APPLICATION NUMBER: US/10/634,548
PRIORITY FILING DATE: 2003-08-05
PRIORITY FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.2
SEQ ID NO 49
LENGTH: 657

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; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-634-548-49

Query Match      51.5%; Score 791.5; DB 4; Length 657;
Best Local Similarity 51.1%; Pred. No. 2.3e-73;
Matches 159; Conservative 60; Mismatches 81; Indels 11; Gaps 4;

Oy 2 AATPLSPINHQLCR---FGNNSL-----TTHRFCSGFLISSPCFICLT-GMGSAATOLRA 53
Db 346 AARPVDVVRHPFPCSSSVAASSSLLSRKSRLASPAAASMSRRRLVLTGVGAAA---A 402
Oy 54 RRSLSAVATNSLHDVGATVAVLGAVALVLSFESLTKRNVIQOOSLRKLVHLSGL 113
Db 403 PAVAAASATPALRDCAATLLITAGAYSLVRAPDGTARLLIQNSLRKIVHLSGL 462

Oy 114 FVLAMPFSGSTEARYFAAFVPLVNGLRLVINGLSISPSNMLIKSVTEGRAEELKGPL 173
Db 463 FMSWPLFSNSTEARFPAAIVPLNLCIRLLTYGLRLSTDEALVKSVTREKPEEILRGPL 522

Oy 174 FYVALLESVAVFPFRESPIGMSILAMCGGDGIADIMGRKFGSTKIPNPKSMAGSISM 233
Db 523 YVIVLLVSVLVPFMSQSDIGIVLSLMSGGDFADIVGRRYGSALPPEKNKSWIGSISM 582

Oy 234 FIFGFISIALLYYSSLGYLHMMNETLQRYAVMSVATVSESPIPTDQLDNISVPLA 293
Db 583 FISGFLSALMLFYSCIGYFTVCMDLALGKALVALAATVVECI PAVDVVDNISVPLA 642

Oy 294 TILAAYLSFGY 304
Db 643 TMLAAYLLFGY 653

RESULT 13
US-10-437-963-179783
; Sequence 179783, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 179783
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_77211C.1.pep
US-10-437-963-179783

Query Match      51.5%; Score 791.5; DB 4; Length 657;
Best Local Similarity 51.1%; Pred. No. 2.3e-73;
Matches 159; Conservative 60; Mismatches 81; Indels 11; Gaps 4;

Oy 2 AATPLSPINHQLCR---FGNNSL-----TTHRFCSGFLISSPCFICLT-GMGSAATOLRA 53
Db 346 AARPVDVVRHPFPCSSSVAASSSLLSRKSRLASPAAASMSRRRLVLTGVGAAA---A 402
Oy 54 RRSLSAVATNSLHDVGATVAVLGAVALVLSFESLTKRNVIQOOSLRKLVHLSGL 113
Db 403 PAVAAASATPALRDCAATLLITAGAYSLVRAPDGTARLLIQNSLRKIVHLSGL 462

Oy 114 FVLAMPFSGSTEARYFAAFVPLVNGLRLVINGLSISPSNMLIKSVTEGRAEELKGPL 173

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; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-634-548-49

Query Match      51.5%; Score 791.5; DB 4; Length 803;
Best Local Similarity 51.1%; Pred. No. 3e-73;
Matches 159; Conservative 60; Mismatches 81; Indels 11; Gaps 4;

Oy 2 AATPLSPINHQLCR---FGNNSL-----TTHRFCSGFLISSPCFICLT-GMGSAATOLRA 53
Db 492 AARPVDVVRHPFPCSSSVAASSSLLSRKSRLASPAAASMSRRRLVLTGVGAAA---A 548
Oy 54 RRSLSAVATNSLHDVGATVAVLGAVALVLSFESLTKRNVIQOOSLRKLVHLSGL 113
Db 549 PAVAAASATPALRDCAATLLITAGAYSLVRAPDGTARLLIQNSLRKIVHLSGL 608

Oy 114 FVLAMPFSGSTEARYFAAFVPLVNGLRLVINGLSISPSNMLIKSVTEGRAEELKGPL 173
Db 609 FMSWPLFSNSTEARFPAAIVPLNLCIRLLTYGLRLSTDEALVKSVTREKPEEILRGPL 668

Oy 174 FYVALLESVAVFPFRESPIGMSILAMCGGDGIADIMGRKFGSTKIPNPKSMAGSISM 233
Db 669 YVIVLLVSVLVPFMSQSDIGIVLSLMSGGDFADIVGRRYGSALPPEKNKSWIGSISM 728

Oy 234 FIFGFISIALLYYSSLGYLHMMNETLQRYAVMSVATVSESPIPTDQLDNISVPLA 293
Db 729 FISGFLSALMLFYSCIGYFTVCMDLALGKALVALAATVVECI PAVDVVDNISVPLA 788

Oy 294 TILAAYLSFGY 304
Db 789 TMLAAYLLFGY 799

RESULT 14
US-10-634-548-48
; Sequence 48, Application US/10634548
; Publication No. US20040045051A1
; GENERAL INFORMATION:
; APPLICANT: No. US20040045051A1ris, Susan R
; APPLICANT: Lincoln, Kim
; APPLICANT: Abad, Mark Scott
; APPLICANT: Eilers, Robert
; APPLICANT: Hartsuyker, Karen Kindle
; APPLICANT: Hirschberg, Joseph
; APPLICANT: Karunanandaa, Balasubrajini
; APPLICANT: Moshiri, Farnad
; APPLICANT: Stein, Joshua C.
; APPLICANT: Valentini, Henry E.
; APPLICANT: Venkatesh, Tyamagondlu V.
; TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof
; FILE REFERENCE: Ren-01-125
; CURRENT APPLICATION NUMBER: US/10/634,548
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: us 60/400,689
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-634-548-48

```

RESULT 15

US-10-437-963-179784
; Sequence 179784, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT PILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 179784
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_77212C.1.pdp
US-10-437-963-179784

Query Match 51.5%; Score 791.5; DB 4; Length 803;
Best Local Similarity 51.1%; Pred. No. 3e-73;

Matches 159; Conservative 60; Mismatches 81; Indels 11; Gaps 4;

QY 2 AATPLSPINHOLCR---FGNNSL---TTRPCSPGFLISSPCFGLT-GKGSATQURA 53
DB 492 AAAPPVVVRHPCSSSVAASSSLRSKRSRLASPAAAASMRRLVLGVGAAA---A 548
QY 54 RRSLSGAVATNSLHDVCAVAVLGCAYALVSPESITKENVIQQSIRKLVHILGGL 113
DB 549 PAVALLASATPALRDCAATLLITAGAYSLVRAFDGLTARRLLIIONSRKIYHVLGVL 608
QY 114 FVLAMPFGSGSTEARYFAFVPLVNGRLVINGLSISPSMLIKSVTREGRAEELKGPL 173
DB 609 FMSMPLEFSNSTEARFPAIVPLANCIRLLTYGLRISTDEALVKSIVREGPEELRGPL 668
QY 174 FYVALLPFSAVFPWRRESPIGMI SLAMCGGDIADIMGRKFGSTKIPYPRKSWAGSISM 233
DB 669 YVIVLVLSVLPFWRQSPIGIVSLSMMSGDGPADIVGRRYGSAKL PENENKSWIGSISM 728
QY 234 FIFGFFISIALLYTYSIGYIHNWETLQRYVAMVSMVATVESLPITDQDDNISVPLA 293
DB 729 FISGFLLSALMLFYFSCIGYPTVCMDLALGRLALVALAATVCEIPVNDVVDNISVPLA 788
QY 294 TILAAYLSFGY 304
DB 789 TMLAAYLLFGY 799

Search completed: March 16, 2006, 19:53:26
Job time : 80 secs

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US-11-096-568A-19560
 ; Sequence 19560, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nikolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO 19560
 ; LENGTH: 268
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(268)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12373618
 US-11-096-568A-19560

Query Match 50.5%; Score 776; DB 7; Length 268;
 Best Local Similarity 58.8%; Pred. No. 9,4e-62;
 Matches 143; Conservative 52; Mismatches 48; Indels 0; Gaps 0;

QY 60 SAVATNSLHDVGATVAVLGGAYALVLSFESLTKRNVIOQSLSRKLVHLSGLFVLAMP 119
 DB 18 AAAAPPAVLDGAVTVLITAGVSLVRVDELTERRLIKSLSRKVVHLSGLFVMSWP 77
 QY 120 IFSGSTEARYFAAFVPLVNGRLVINGLSISPSNMLIKSVTRGAEELKGPLFYVAL 179
 DB 78 LFSNSTEARVFAAVVPEPLNSMRLIYGLRLYTDALVKSVTREGKPEELRGPLYVVAL 137
 QY 180 LPSAVFPFRESITGMSLMMCGGDIADIMGRKGSITKIPNPKKSWAGSISMTIFEF 239
 DB 138 LFSVIVFWRRESPIGIVLSMMSGGDFADIVGRYGSALPFRKKSWAGSISMTISGFL 197
 QY 240 ISALLYYYSLSGLYHMMWETTLQRYVAMSVWATVESLPITDQDDNISVPLATILAA 299
 DB 198 LSAMMLYFSSLSGIYDIVWEALGKLVLAALVAVVECPVTEVDNISVPLATMLVAF 257
 QY 300 LSF 302
 DB 258 LLF 260

RESULT 3
 US-11-096-568A-19561
 ; Sequence 19561, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nikolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO 19561
 ; LENGTH: 196
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(196)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12373619
 US-11-096-568A-19561

Query Match 41.4%; Score 636; DB 7; Length 196;
 Best Local Similarity 61.8%; Pred. No. 1.8e-49;
 Matches 115; Conservative 38; Mismatches 33; Indels 0; Gaps 0;
 QY 117 AMPIFSSTEARYFAAFVPLVNGRLVINGLSISPSNMLIKSVTRGAEELKGPLFYV 176

DB :||| ||||| ||| :||| :||| ||||| :||| |||
 3 SWPLFSNSTEARVFAAVVPEPLNSMRLIYGLRLYTDALVKSVTREGKPEELRGPLYV 62
 QY 177 LALFSAVFPFRESIPICMISLMMCGGDIADIMGRKGSITKIPNPKKSWAGSISMTIF 236
 DB 63 LVLLFSVIVFWRRESPIGIVLSMMSGGDFADIVGRYGSALPFRKKSWAGSISMTIS 122
 QY 237 GPFISALLYYYSLSGLYHMMWETTLQRYVAMSVWATVESLPITDQDDNISVPLATIL 296
 DB 123 GFLLSAMMLYFSSLSGIYDIVWEALGKLVLAALVAVVECPVTEVDNISVPLATML 182
 QY 297 AAYLSF 302
 DB 183 VAFLLF 188

RESULT 4
 US-11-096-568A-1771
 ; Sequence 1771, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nikolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO 1771
 ; LENGTH: 259
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(259)
 ; OTHER INFORMATION: Ceres Seq. ID no. 15178975
 US-11-096-568A-1771

Query Match 39.9%; Score 613; DB 7; Length 259;
 Best Local Similarity 43.9%; Pred. No. 2.8e-47;
 Matches 125; Conservative 50; Mismatches 54; Indels 56; Gaps 4;

QY 29 SPGFLL--SSPCFGLTGMGSATQLRARSLIS-----SAVATNSLHDVGATVAV 77
 DB 12 SPNSLLSRSPFAVLAAPSPGSSWR--RRLILGVTPAVALAAAPPAVLDGAVTVLI 70
 QY 78 LGAVALVLSFESLTKRNVIOQSLSRKLVHLSGLFVLAMPISGSTEARYFAAFVPLV 137
 DB 71 TAGVSLVRVDELTERRLIKSLSRKVVHLSGLFVMSWP----- 114
 QY 138 NGLRLVINGLSISPSNMLIKSVTRGAEELKGPLFYVALLFSVFPWRESPIGIMISL 197
 DB 115 -----RELLRGPLYVVLVLFVFWRESPIGIVSL 146
 QY 198 AMMCGGDIADIMGRKGSITKIPNPKKSWAGSISMTIFGPFISALLYYYSLSGLYHMM 257
 DB 147 SMMSGGDFADIVGRYGSALPFRKKSWAGSISMTISGFLLSAMMLYFSSLSGIYDI 206
 QY 258 WETTLQRYVAMSVWATVESLPITDQDDNISVPLATILAAVLSF 302
 DB 207 WEALGKLVLAALVAVVECPVTEVDNISVPLATMLVAFLLF 251

RESULT 5
 US-11-096-568A-1770
 ; Sequence 1770, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nikolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01
 NUMBER OF SEQ ID NOS: 34471
 SEQ ID NO 1770
 LENGTH: 270
 TYPE: PRT
 ORGANISM: Zea mays subsp. mays
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)-(270)
 OTHER INFORMATION: Cereb Seq. ID no. 15178974
 US-11-096-568A-1770

Query Match 39.9%; Score 613; DB 7; Length 270;
 Best Local Similarity 43.9%; Pred. No. 3e-47;
 Matches 125; Conservative 50; Mismatches 54; Indels 56; Gaps 4;

QY 29 SPGLI--SSPCFGLTGMGATOLRARSLIS-----SAVATSLHDVATVAV 77
 DB 23 SPNLSLSRSPHAAVLAPSPGSSMR-RRLILGVCTPAVAAALAAAPAVLQDGVATLI 81
 QY 78 LGGAVLVLPESLTKRVNIOQSLSRKLVHLSGLLFTLAMPISGSTEAFVPAFVPLV 137
 DB 82 TAGAVSLVRVDELTERRLIKSLSRKVVHLSGLVFMSSWPLF----- 125
 QY 138 NGALVINGLISIPNSMLIKSVTREGRAEELKGPLFYVALLFSVAFWRESPIGMISL 197
 DB 126 -----RELKGPLYVALVLSVLFVWRESPIGLIVSL 157
 QY 198 AMMGCGDIADIMGRKFGSTKIPYNPBKSWAGSISMPFEGFISIALIYYSSIGYLMN 257
 DB 158 SMWGGGDFADIVGRYGSALLPFRKKSWAGSISMPISGFLISMMLLYSSIGYIDVI 217
 QY 258 WETLQVAVNSVATVYESLPITDOLDNISVPLATILAYLSF 302
 DB 218 WEELGKLALVALAAYVECVPTREVVDNISVPLATVLAFLIF 262

RESULT 6

US-11-096-568A-1772
 Sequence 1772, Application US/11096568A
 Publication No. US20060048240A1
 GENERAL INFORMATION:
 APPLICANT: Alexandrov, Nikolai et al.
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 TITLE OR INVENTION: Theby
 FILE REFERENCE: 2750-1592PUS2
 CURRENT APPLICATION NUMBER: US/11/096,568A
 CURRENT FILING DATE: 2005-04-01
 NUMBER OF SEQ ID NOS: 34471
 SEQ ID NO 1772
 LENGTH: 224
 TYPE: PRT
 ORGANISM: Zea mays subsp. mays
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)-(224)
 OTHER INFORMATION: Cereb Seq. ID no. 15178976
 US-11-096-568A-1772

Query Match 39.7%; Score 610; DB 7; Length 224;
 Best Local Similarity 47.7%; Pred. No. 4.4e-47;
 Matches 116; Conservative 45; Mismatches 38; Indels 44; Gaps 1;

QY 60 SAVATSLHDVATVAVLGGAVLVLPESLTKRVNIOQSLSRKLVHLSGLLFTLAMP 119
 DB 18 AAAAPAVLQDGVATVITAGAYSLVRVDELTERRLIKSLSRKVVHLSGLVFMSSWP 77
 QY 120 IFSGSTEARVPAFVPLVNGALVINGLISIPNSMLIKSVTREGRAEELKGPLFYVAL 179
 DB 78 LF-----RELKGPLYVALV 93
 QY 180 LFSVAFWRESPIGMISLMMCGGDIADIMGRKFGSTKIPYNPBKSWAGSISMPFISGF 239

DB 94 LFSVAFWRESPIGIVLSMMWGGDFADIVGRYGSALKLPFRKKSWAGSISMPISGFL 153
 QY 240 ISIALIYYSSIGYLMNWEETLQVAVNSVATVYESLPITDOLDNISVPLATILAY 299
 DB 154 LSAMMDYFSSLYIDVIMBEGALKALVALAATVVECVPTREVVDNISVPLATMLVAF 213
 QY 300 LSF 302
 DB 214 LIF 216

RESULT 7

US-11-096-568A-14812
 Sequence 14812, Application US/11096568A
 Publication No. US20060048240A1
 GENERAL INFORMATION:
 APPLICANT: Alexandrov, Nikolai et al.
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 TITLE OR INVENTION: Theby
 FILE REFERENCE: 2750-1592PUS2
 CURRENT APPLICATION NUMBER: US/11/096,568A
 CURRENT FILING DATE: 2005-04-01
 NUMBER OF SEQ ID NOS: 34471
 SEQ ID NO 14812
 LENGTH: 302
 TYPE: PRT
 ORGANISM: Zea mays subsp. mays
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)-(302)
 OTHER INFORMATION: Cereb Seq. ID no. 12336654
 US-11-096-568A-14812

Query Match 36.6%; Score 562.5; DB 7; Length 302;
 Best Local Similarity 41.4%; Pred. No. 1.1e-42;
 Matches 115; Conservative 53; Mismatches 101; Indels 9; Gaps 4;

QY 28 CSPGFLISSPCFGLTGMGATOLRARSLISAV---ATNSLHDVATVAVLGGAVL 84
 DB 31 CAP---RSICFRRRSRLAAE-RTRRPTVAAALISLEGALHDUSAVVGGVALAL 85
 QY 85 VLSFESLTKRVNIOQSLSRKLVHLSGLLFTLAMPISGSTEAFVPAFVPLVNGALRIYI 144
 DB 86 LKPFEBELAKGVFPQKLSRKLVHLSGLVFLFPLFSSGVTTFPLAALACVNIIRLL 145
 QY 145 NGLSIPNSMLIKSVTREGRAEELKGPLFYVALLFSVAFWRESPIGMISLMMCGGD 204
 DB 146 LGGLMKKNEMAVKMSRSGDYRELLKGPLYAAATITFATSLMRTSPVALIALICNLGAD 205
 QY 205 GIADIMGRKFGSTKIPYNPBKSWAGSISMPFEGFISIALIYYSSIGYLMNWEETLQ 264
 DB 206 GIADVGRRLGKELPYNPNKSYAGSIAMAVAGFLAVGWVHYRHTGFIETWYALS- 264
 QY 265 VAVTSMVATVYESLPITDOLDNISVPLATILAYLSF 302
 DB 265 PLVVSVAALVYESHPISTEIDDNITVLTSTVGSLLIF 302

RESULT 8

US-11-096-568A-14813
 Sequence 14813, Application US/11096568A
 Publication No. US20060048240A1
 GENERAL INFORMATION:
 APPLICANT: Alexandrov, Nikolai et al.
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 TITLE OR INVENTION: Theby
 FILE REFERENCE: 2750-1592PUS2
 CURRENT APPLICATION NUMBER: US/11/096,568A
 CURRENT FILING DATE: 2005-04-01
 NUMBER OF SEQ ID NOS: 34471
 SEQ ID NO 14813
 LENGTH: 247
 TYPE: PRT

ORGANISM: Zea mays subsp. mays
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(247)
 OTHER INFORMATION: Cereals Seq. ID no. 12336655
 US-11-096-568A-14813

Query Match 35.8%; Score 549.5; DB 7; Length 247;
 Best Local Similarity 43.6%; Pred. No. 1.2e-41;
 Matches 106; Conservative 47; Mismatches 89; Indels 1; Gaps 1;

QY 60 SAVATNSLHDVGVATVAVLGGAYALVLSFESITKKNVITQGSLSRKLVIHLSGLLFLVLAAP 119
 DB 6 SLBGGALAHDLGSAVTVGVVALMLLKFFBELAKKGVQKLSRKLVIHISGLVFWMLFWP 65
 QY 120 IFSGSTERKRYFAAFPLVNGRLVINGLSISPSNMLISVTRREGAEELKGPLFYVAL 179
 DB 66 LFSSGMYTPFLAALAPGVNIIRMLLGLGLMKNEAMVKSMSGSDYRELKGPLFYATY 125
 QY 180 LFSAVFMRSPICMISLMMCGGDIADIMGRKFGSTKIPYNPKSMAGSISMFIFGPF 239
 DB 126 TFAISLMTKRTSPVALICNLGAGDIADVGRRLGKRLPYNPKSYAGSIAMAVAGFL 185
 QY 240 ISALLYYSSLSGLYLMNMETTLQRYAVSMVAVVESLPITDLDNISVPLATILAA 299
 DB 186 ASVGVMHFHTFGFIEETWYMLS-FLVVSVAALVESHPISTELDNLVLTLSFLVGS 244
 QY 300 LSF 302
 DB 245 LIF 247

RESULT 9

US-11-096-568A-14318
 ; Sequence 14318, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nickolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO 14318
 ; LENGTH: 152
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(152)
 ; OTHER INFORMATION: Cereals Seq. ID no. 3626195
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (7)..(7)
 ; OTHER INFORMATION: Xaa is any aa, unknown or other
 US-11-096-568A-14318

Query Match 30.9%; Score 475; DB 7; Length 152;
 Best Local Similarity 62.5%; Pred. No. 2.8e-35;
 Matches 85; Conservative 29; Mismatches 22; Indels 0; Gaps 0;
 QY 167 ELKGLPLFYVALLSAVFMRSPICMISLMMCGGDIADIMGRKFGSTKIPYNPKS 226
 DB 9 ELKGLPLFYVALLSAVFMRSPICMISLMMCGGDIADIMGRKFGSTKIPYNPKS 68
 QY 227 MAGSISMFIFGFIISLALYYSSLSGLYLMNMETTLQRYAVSMVAVVESLPITDLD 286
 DB 69 MAGSISMFIFGFIISLALYYSSLSGLYLMNMETTLQRYAVSMVAVVESLPITDLD 128
 QY 287 NISVPLATILAAVLSF 302
 DB 129 NISVPLATILAAVLSF 144

RESULT 10

US-11-096-568A-14814
 ; Sequence 14814, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nickolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO 14814
 ; LENGTH: 187
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(187)
 ; OTHER INFORMATION: Cereals Seq. ID no. 12336656
 US-11-096-568A-14814

Query Match 27.5%; Score 422.5; DB 7; Length 187;
 Best Local Similarity 41.0%; Pred. No. 1.7e-30;
 Matches 77; Conservative 41; Mismatches 69; Indels 1; Gaps 1;

QY 115 VLAMPISGSTERKRYFAAFPLVNGRLVINGLSISPSNMLIKSVTRREGAEELKGPLF 174
 DB 1 MLFMPLFSSGMYTPFLAALAPGVNIIRMLLGLGLMKNEAMVKSMSGSDYRELKGPLY 60
 QY 175 VVALLSAVFMRSPICMISLMMCGGDIADIMGRKFGSTKIPYNPKSMAGSISMF 234
 DB 61 YVATITRATSLMTKRTSPVALICNLGAGDIADVGRRLGKRLPYNPKSYAGSIAMA 120
 QY 235 IFGFIISLALYYSSLSGLYLMNMETTLQRYAVSMVAVVESLPITDLDNISVPLAT 294
 DB 121 VAGFIASGVVMHFHTFGFIEETWYMLS-FLVVSVAALVESHPISTELDNLVLTLS 179
 QY 295 ILAAVLSF 302
 DB 180 FLVGS LIF 187

RESULT 11

US-11-096-568A-14319
 ; Sequence 14319, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nickolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO 14319
 ; LENGTH: 112
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(112)
 ; OTHER INFORMATION: Cereals Seq. ID no. 3626196
 US-11-096-568A-14319

Query Match 22.5%; Score 346; DB 7; Length 112;
 Best Local Similarity 59.6%; Pred. No. 5.7e-24;
 Matches 62; Conservative 23; Mismatches 19; Indels 0; Gaps 0;
 QY 199 MCGGDIADIMGRKFGSTKIPYNPKSMAGSISMFIFGFIISLALYYSSLSGLYLMNM 258

Db 1 MMSGDGDGADIVGRRGYSKLPFNRRKSKWAGSISMFISGILLSMMMLYFSSLGIVDIW 60

Qy 259 ETTIQRVAMVSMVATVSESLPTDOLDNISVPLATITLAATYSP 302

Db 61 EALGKALVALVAATVCEVPTVEVDNISVPLATMLVAFLLP 104

RESULT 12

US-11-096-568A-14320

Sequence 14320, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-determined DNA fragments and corresponding polypeptides

TITLE OF INVENTION: Thedy

FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 14320

LENGTH: 111

TYPE: PRT

ORGANISM: Zea mays subsp. mays

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)_(111)

OTHER INFORMATION: Ceres Seq. ID no. 3626197

US-11-096-568A-14320

Query Match 22.2%; Score 341; DB 7; Length 111;
Best Local Similarity 59.2%; Pred. No. 1,66-23;

Matches 61; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

Qy 200 MCGDGDGADIVGRRGYSKLPFNRRKSKWAGSISMFISGILLSMMMLYFSSLGIVDIW 259

Db 1 MMSGDGDGADIVGRRGYSKLPFNRRKSKWAGSISMFISGILLSMMMLYFSSLGIVDIW 60

Qy 260 TTLDQVAMVSMVATVSESLPTDOLDNISVPLATITLAATYSP 302

Db 61 EALGKALVALVAATVCEVPTVEVDNISVPLATMLVAFLLP 103

RESULT 13

US-11-087-099-1186

Sequence 1186, Application US/11087099

Publication No. US20060041961A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant Improvement

FILE REFERENCE: 38-21(53450)B RP

CURRENT APPLICATION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 1186

LENGTH: 477

TYPE: PRT

ORGANISM: Chlorobium tepidum T15

US-11-087-099-1186

Query Match 8.6%; Score 132.5; DB 7; Length 477;
Best Local Similarity 28.0%; Pred. No. 0,00033;

Matches 53; Conservative 37; Mismatches 74; Indels 25; Gaps 11;

Qy 129 YEAA-PVPLVNGRLVINGISISPNMLIKS-----VTRGRABELIK-GPLFYVIAL 180

Db 11 YFSNFYPLAALFPAVVGVL-VSLAKGILQSLHGPVVTGG--BRVSYGYPVLFPVLF 67

Qy 181 FSAVFFWRESF-IGMISLMMCGGDIADINGRKSGTKIP--XNPRKSWAGSISMFIFG 237

Db 68 LQALFLMEHWHWIIQISMLVIGIDALALVGTAAAGSHIENLTYSKISGSSAMPTSS 127

Qy 238 FFI-SIALLYYSSY--GYLHMNETTLQVAMVSMVATVSESLPTDOLD---DNISVP 291

Db 128 LVIVSVIFVRDPAFTGVLQGPVWKLLALALLALVTVAEAL-----LSMGLDNLP 182

Qy 292 LATILAAYL 300

Db 183 LAIAVYLYV 191

RESULT 14

US-10-793-626-2168

Sequence 2168, Application US/10793626

Publication No. US20050255478A1

GENERAL INFORMATION:

APPLICANT: KIMBERLY, WILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

TITLE OF INVENTION: P31480US

FILE REFERENCE: P31480US

CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT FILING DATE: 2004-03-04

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patent Ver. 2.1

SEQ ID NO 2168

LENGTH: 383

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-10-793-626-2168

Query Match 6.4%; Score 98.5; DB 6; Length 383;
Best Local Similarity 19.9%; Pred. No. 0,027;

Matches 67; Conservative 49; Mismatches 103; Indels 117; Gaps 13;

Qy 13 QLCFRGNSLTTNRFCSPGFLISSPCFGLTGMSATQLRARRSLISAVATNSLHDVG 72

Db 61 QIVFKSSTLTNIGFET---IISNP---WLTVLQGFILITVIVMLGVEKG--LEKAS 112

Qy 73 ATVAVAGAAVAVUSFESLTGRANVQ-----QSLSKLVHISGLFLVLAAPFES 122

Db 113 KIMPLLEFLIIVVAOSTLLEGALGVRVYLLQPRVDM5-----IQGVLPALQGSFT 166

Qy 123 ---GSTEARVPAFVP-----LVNGRLVINGISISPNMLISVTRGRAB 166

Db 167 LSLDTTGMITYASAPKMTIKSALSLVWNLISVLAGLAFPAKLTBTGQEG--- 223

Qy 167 ELKGPFLFYVALLFSAVFFWRESPIGMISLMMCGDGDADINGRKSGTKIPNPKS 226

Db 224 ---PGLLPKVLPLVSEWTF----- 240

Qy 227 WAGSISMFIFGFFISIALITYSSLGYLMMW-----ETTLQVAMVSMVATVSESLP 279

Db 241 --GTFYFIFLPLFAL--TSSISLLELVNSFTKNDNSKQKVALIGSLVLEFISIP 296

Qy 280 IT-----DOLD---DNISVPLATI 295

Db 297 ATLSFSSLSHURFAGATTFDMDFIVSNITLPLGAL 332

RESULT 15

US-11-092-140-6

Sequence 6, Application US/11092140

Publication No. US20050262590A1

GENERAL INFORMATION:

APPLICANT: Subramaniam, S.; Slater, S.; Karberg, K.; Chen, R.; Valentini, H.; Wong, Y.

TITLE OF INVENTION: Nucleic Acid Sequences to Proteins Involved in Tocopherol Synthesis

FILE REFERENCE: 16515,054

CURRENT APPLICATION NUMBER: US/11/092,140

CURRENT FILING DATE: 2005-03-29

PRIOR APPLICATION NUMBER: US/09/688,069

PRIOR FILING DATE: 2000-10-14

NUMBER OF SEQ ID NOS: 114

SEQ ID NO 6

; LENGTH: 431
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis sp.
 US-11-092-140-6

Query Match 6.3%; Score 97; DB 7; Length 431;

Best Local Similarity 21.9%; Pred. No. 0.42;
Matches 76; Conservative 50; Mismatches 121; Indels 100; Gaps 18;

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QY      1 MAATLP--LSPINQLCRFGNNSLTTRFCSPGFLISSPCFGLTGWGS-ATQLRARS 56
      16 VSSSLPNPRLIPWSREL-----AVNSFSQPPVSTESTAKLGITGVSDNRVFATAT 68
QY      57 LISSAVATNSLHDVATVAVLGAYA-----LVLIS 87
      69 AAATATATTGERISSRVALLAGLGHYARCWELSKAKLSMLVVAATSGTYLLGTGNAIS 128
QY      88 FESL-----TKENVIOQ-----SLSRKLVIHL-SGLLFV--LAMPFESGS 124
      129 FPGLCYTCAGTMMIINASANSINQIPEISNDSKMKRTMLRPLPSGRISVPHAVAMATTIAGA 188
QY      125 TEARYFAAFV-PIVNGL---RIVNGLSISPNSML-----IKSVTRGRABEEL----- 169
      189 SGACILASKTNMLAAGLASANLVYAFTYTPKQLHPINTWGAIV--GALPPLGMAAA 246
QY      170 KGPLFYVALLPSAVFFWRESPIGMSISLAMCGDGIADIMGRKFGSTKIPYPRKSWAG 229
      247 SGOISYNSMILPALYFW-QIP-HMALAHLGRNDYAG--GYKMLSLFDPGKR----- 297
QY      230 SISMFIFGFISIAL-LYYSSLGYLMMNMETTLQRYAMVSMVATV 274
      298 -----IAVALRNCFYMIPLGFIAYDWGLTSSWPCLESTLTL 335
Db
  
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Search completed: March 16, 2006, 19:53:47
Job time : 15 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: March 16, 2006, 19:54:00 ; Search time 7741 Seconds

(without alignments)
2232.323 Million cell updates/sec

Title: US-10-634-548-2

Perfect score: 1536
Sequence: 1 MAATLPSPINHQCRCRGN.....DDNISVPLATIAAYLSFGY 304

Scoring table:

BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blowsum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcr -NORNAEXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss02h
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1536	100.0	1004	15 BT021123	BT021123 Arabidops
2	1531	99.7	1072	15 BT004006	BT004006 Arabidops
3	1523	99.2	1091	15 AY085036	AY085036 Arabidops

4	1299.5	84.6	93045	15 ATT32M21	AL162875 Arabidops
5	569.5	37.1	1002	15 AK061265	AK061265 Oryza sat
6	561.9	35.9	95419	15 OSIG00051	AL732356 Oryza sat
7	551	35.9	110000	15 AP008210_342	Continuation (343
8	551	35.9	190432	15 OSUN00032	Continuation (343
9	536.5	34.9	1218	15 AK110748	AK110748 Oryza sat
10	531.5	34.6	1211	15 AK176090	AK176090 Arabidops
11	530.5	34.5	1360	15 AK176217	AK176217 Arabidops
12	526.5	34.3	1162	15 AY087555	AY087555 Arabidops
13	526.5	34.3	3143	15 AK065924	AK065924 Oryza sat
14	505	32.9	1059	15 AK109049	AK109049 Oryza sat
15	455	29.6	110000	14 CR954207_0	CR954207 OatReococ
16	403.5	26.3	110000	14 CR954207_1	Continuation (2 of
17	369	24.0	81672	15 AB020755	AB020755 Arabidops
18	363	23.6	110000	15 AP008207_355	Continuation (356
19	363	23.6	143515	15 AP003252	AP003252 Oryza sat
20	357.5	23.3	110000	15 AP008217_002	Continuation (3 of
21	357.5	23.3	160673	15 CNS08CDR	AK063069 Oryza sat
22	356	23.2	436	15 AK063069	Continuation (7 of
23	356	23.2	110000	14 AP006500_06	Continuation (17 of
24	348.5	22.7	518	10 BV151383	BV151383 PZA02133-
25	347.5	22.6	529	10 BV151386	BV151386 PZA02133-
26	344.5	22.4	513	10 BV151382	BV151382 PZA02133-
27	344.5	22.4	516	10 BV151377	BV151377 PZA02133-
28	343.5	22.4	513	10 BV151378	BV151378 PZA02133-
29	343.5	22.4	513	10 BV151379	BV151379 PZA02133-
30	343.5	22.4	515	10 BV151385	BV151385 PZA02133-
31	339.5	22.1	506	10 BV151376	BV151376 PZA02133-
32	339.5	22.1	506	10 BV151384	BV151384 PZA02133-
33	334.5	21.8	110000	15 AP008218_002	Continuation (3 of
34	334.5	21.8	152222	15 CNS08CDR	BX000494 Oryza sat
35	332.5	21.0	493	10 BV151387	BV151387 PZA02133-
36	296.5	19.3	485	10 BV151381	BV151381 PZA02133-
37	289.5	18.8	477	10 BV151380	BV151380 PZA02133-
38	289.5	18.8	14603	2 AC116989	AC116989 Dictyoste
39	234	15.2	110000	1 AB006470_18	Continuation (19 o
40	203	13.2	110000	1 BA000019_18	Continuation (19 o
41	195	12.7	15085	1 AB000745	AB000745 Aquifex a
42	195	12.7	110000	1 BA000022_34	Continuation (35 o
43	184.5	12.0	11925	1 AB001013	AB001013 Archaeogl
44	180	11.7	110000	1 AB017261_13	Continuation (14 o
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ALIGNMENTS

RESULT 1
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LOCUS Arabidopsis thaliana 1004 bp mRNA linear PLN 05-MAR-2005
DEFINITION Arabidopsis thaliana At5g04490 gene, complete cde.
ACCESSION BT021123
VERSION BT021123.1 GI:60543320
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana (chale crees)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE
AUTHORS Kim,C.J., Chen,H., Cheuk,R., Shinn,P. and Ecker,J.R.
TITLE Arabidopsis ORF clones
JOURNAL Unpublished
2 (bases 1 to 1004)

REFERENCE
AUTHORS Kim,C.J., Chen,H., Cheuk,R., Shinn,P. and Ecker,J.R.
TITLE Direct Submission
JOURNAL Submitted (05-MAR-2005) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA

FEATURES
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CDS

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/notes="unknown protein"
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/product="At5g04490"
/protein_id="AAK2258.1"
/db_xref="GI:60543321"
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MSATQLRARSLISSAVATLSLHDGATVAVIGAVAVLSTESLTKNVQOQSL
KLVHILSLFLVAMPFSGSTEARFAAPLVNGLRVYINGLSIPNSMLKSYT
REGARSLKGLPYVALIFSAVFPWRSPFGIMISLMMCGGPGDIADIGRKRSYTK
IPVPRKSMAGSISMPFGPISIALIYYSLSGLYMMNETTILQRAVMSMAVIVE
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ORIGIN

Alignment Scores:

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Pred. No.:      8.48e-129      Length:      1004
Score:          1536.00      Matches:      304
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    100.0%      Indels:      0
DB:             15      Gaps:      0

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US-10-634-548-2 (1-304) x BT021123 (1-1004)

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Qy 1 MetAlaAlaThrLeuProLeuSerProIleAaNHISGInLeuCYAaRphGlyVaNHsN 20
Db 19 ATGGCAGAACCTTAACCTCTATCTCCGATCAATCATCATGTTGTGCGGTCGGGAACAAC 78
Qy 21 SerLeuThrThrHisArgPheCysSerProGlyPheLeuIleSerSerProCYaPheHle 40
Db 79 TCTTGGACACTCACCGGTCCTGTTCTCTCGCTTCGATTCTTCTCTGTTTCATY 138
Qy 41 GlyLeuThrGlyMetGlySerAlaThrGInLeuAaRgaAaRgaSerLeuIleSerSer 60
Db 139 GGTTCGACCGGAATGGCTCTGCTACTGATCAAGTACGCTGCTGCTCTGATCTCTTCA 198
Qy 61 AlaValAlaThrAaSerLeuLeuHisAaPValGlyAlaThrValAlaValLeuGly 80
Db 199 GCATGTCGACGAATTCGCTGTTGATGATCGTCGACGACCAACGTCGCTTGGTGA 258
Qy 81 AlaTyrAlaLeuValLeuSerPheGlnSerLeuThrIaRgaAaNHISGInLeuSer 100
Db 259 GCATACGGCTGTGCTTAAGCTTCAGAGCTTCACCAAGCAAAAGTCATTCACAGAGT 318
Qy 101 LeuSerArgIaLeuValHisIleLeuSerGlyLeuLeuPheValLeuAlaTrrProIle 120
Db 319 TTGAGCAGAAAGCTTGTCATTAATCTCAGAGTCTTTCGTAATCTTGGCGTCAATC 378
Qy 121 PheSerGlySerThrGInAlaArgTyrPheAlaAaPheValProLeuValAaNHISG 140
Db 379 TTCAGCGGATGACACGAGGCTCGAATCTTGTGCTTGTTCGCTTGAATGGCTTA 438
Qy 141 ArgLeuValIleAaNHISGLeuSerIleSerProAaSerMetLeuIleIaSerValThr 160
Db 439 AGGCTGTATTATTAACGACTATCAATTCACCAATTCGATGCTAATCAATCCGTCA 498
Qy 161 ArgGInGlyArgAlaGInGlyLeuLeuGlyGlyProLeuPheTyrValLeuAlaLeuLeu 180
Db 499 AGAGAAAGGAGAGCAGAAAGAGTGTAAAGTCTTGTCTCAAGTCTTCTTCTT 558
Qy 181 PheSerAlaValPhePheTrrPArgIaSerProIleGlyMetIleSerLeuAlaMetNec 200
Db 559 TTCCTCGCGGTTTCTTCTCGAGAGAGTCTCTATCGGTATGATCTCGTTAGCAATGATG 618
Qy 201 CysGlyGlyAaRphGlyIleAlaAaPValMetGlyArgIaSerPheGlySerThrIaLeuPro 220
Db 619 TGTGTGGCGATGAGATAGCTGATATTAATGAGGACGTAAGTTGGGTCAACTAAGATACCT 678

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Qy 221 TyrAaProArgIaSerTrrPAlaGlySerIleSerMetPheIlePheGlyPhePheIle 240
Db 679 TACACCCAGAAAGAGTTGGCGCAGAGCATCTCCATGTTCACTTCCTGCTTCATC 738
Qy 241 SerIleAlaLeuLeuTyrTrrTrrSerSerLeuGlyTyrLeuHisMetAaNHISGInThr 260
Db 739 TCCATCCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 798
Qy 261 ThrLeuGInArgValAlaMetValSerMetValAlaThrValValGInSerLeuProIle 280
Db 799 ACCTTGACAGAGTAGAGATAGTCTCATGTCGCCACGATGCGATGCTGCTTCCATC 858
Qy 281 ThrAspGInLeuAaPheAaNHISGLeuValProLeuAlaThrIleLeuAlaAaTrrLeu 300
Db 859 ACCGATCAATTAAGCAGCATATTTGCGTCTCTGCGCTACTATTTAGCTGCTTAATTA 918
Qy 301 SerPheGlyTrr 304
Db 919 AGTTTCGATAT 930

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RESULT 2

BT004006

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (14-FEB-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAPL cDNAs: Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shim, P., Southwick, A., Trimp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation based on July 2002 version of the Arabidopsis genome

FEATURES submitted to Genbank. Location/Qualifiers

source 1..1072 /organism="Arabidopsis thaliana" /mol_type="mRNA" /db_xref="taxon:3702" /chromosome="5" /clone="RAP15-38-N13 (R50070)" /ecotype="Columbia" /note="This clone is in a modified pBluescript vector2 (lambda PS) as a BamHI/XhoI insert."

gene 1..1072 /gene="At5g04490"

5' UTR 1..69 /gene="At5g04490"

CDS 70..984 /gene="At5g04490" /codon_start=1 /evidence=experimental /product="unknown protein" /protein_id="AA042044.1" /db_xref="GI:28393229" /translation="MAATLPSPINHOLCFGNNSLTTHRFCSPPFLISSPCFGLTG MGSATQLRARSLISAVATNSLDHGAVALVGAVALVLSPESTLKNVQOQIS RKVHLISGLPLVLPAPIPGSGTEARFAAFVPLVNLRLVINGLISIPMSLTKSVT RGRARSLIKGPLPYVALPSAAYPRBPDIQISLMMCGGDINDMGRKRGSTK IPNPKRSNAGSISMTFGFFISIALYIYSLSGLHMMETTLQRVAMVSVATVVE SLPTDQLDNISVPLATILAAVLSFGY"

misc_difference 289 /gene="At5g04490" /note="compared to genomic sequence resulting in an amino acid sequence difference" /replace="a" 985..1072 /gene="At5g04490"

ORIGIN

3' UTR

Alignment Scores:

Pred. No.: 2.6e-128 Length: 1072

Score: 1531.00 Matches: 303

Percent Similarity: 99.7% Conservative: 0

Best Local Similarity: 99.7% Mismatches: 1

Query Match: 99.7% Indels: 0

DB: 15 Gaps: 0

US-10-634-548-2 (1-304) x EF004006 (1-1072)

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Db 70 ATGGCAGCAACCTTAACCTCTATCTCCATCAATCAATCAATGTTGTCGGTGGGAACAC 129

Qy 21 SerLeuThrThrAlaArgPheCySerProGlyPheLeuIleSerSerProCyPheIle 40

Db 130 TCTTTGACGACTCAACCGGTTCTGTTCTCCGCTGCTTGAATTTCTTCCCTGTTTCAAT 189

Qy 41 GlyLeuThrGlyMetGlySerAlaThrGlnLeuAlaArgAlaArgSerLeuIleSerSer 60

Db 190 GGTTCGACCGAAGGCGCTGCTCACTCACTCACTCACTGCTGCTGCTGCTGCTGCTTCA 249

Qy 61 AlaValAlaThrAsnSerLeuLeuAlaAspValGlyAlaThrValAlaValLeuGlyGly 80

Db 250 GCAGTTCGACGAAATTCGCTTTCATGACGTCGAGAGCCGCGTGGCAGTCTGAGTGA 309

Qy 81 AlaTyrAlaLeuValLeuSerPheGluSerLeuThrIleArgAsnValIleGlnGlnSer 100

Db 310 GCATTCACCGCTTGTCTTAAGCTTCGAGAGTCTCAACGACGAAACGTCATTCACAGAGT 369

Qy 101 LeuSerArgValLeuValAlaIleLeuSerGlyLeuLeuPheValIleAlaTyrProIle 120

Db 370 TTGAGCGAAGAGCTTGTGCAATATCTCAGAGTCTGCTTTCGTAATTCGCGGCCAATC 429

Qy 121 PheSerGlySerThrGlnAlaArgTyrPheAlaAlaPheValProLeuValAsnGlyLeu 140

Db 430 TTCAGCGGATGACACGAGGCTCCATCTTGCTGCTTTTGTTCGTTAGTAAGTGCCTTA 489

Qy 141 ArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMetLeuIleLeuSerValThr 160

Db 490 AGGCTTGTATTTAAACGACATCAATCATTTCCCAATTCGATGCTAAATCCGTCACA 549

Qy 161 ArgGlnGlyArgAlaGlnGlnGlnLeuLeuGlyGlyProLeuPheTyrValAlaLeuLeu 180

Db 550 AGAAGAGGAGACGACGAGAGTTCCTTAAGAGTCTTGTTCATGCTTACGCTTCTT 609

Qy 181 PheSerAlaValPhePheTyrArgGluSerProIleGlyMetIleSerLeuAlaMetMet 200

Db 610 TTCTCTCGGTTTCTTCTCGAGAGAGTCTCCATGCTGTAATGATCTGTTAGCAATATG 669

Qy 201 CysGlyGlyAspGlyIleAlaAspIleMetGlyArgValPheGlySerThrValIlePro 220

Db 670 TGTGTGCGCATGGAATAGCTGATATATGAGAGCTAATGTTGGGTCAACTAATACACT 729

Qy 221 TyrAsnProArgValSerSerTPAlaGlySerIleSerMetPheIlePheGlyPhePhe 240

Db 730 TACAAACCAAGAAAGAGTTCGACGAGAGCAATCTCCATGTTCACTTCGCTTTCATC 789

Qy 241 SerIleAlaLeuLeuTyrTyrTyrSerSerLeuGlyTyrLeuHisMetAsnTyrGluThr 260

Db 790 TCCATCGCATTTACTTACTTACTTACTCAAGCTTCGGTACCTTCACATGAACCTGGAAACG 849

Qy 261 ThrLeuGlnArgValAlaMetValSerMetValAlaThrValValGluSerLeuProIle 280

Db 850 ACCTTGACGAGAGAGAGCAATGCTCAATGTCGCCACGCTAGTCGAGTGCATCAACCATC 909

Qy 281 ThrAspGlnLeuAspAspAsnIleSerValProLeuAlaThrIleAlaAlaTyrLeu 300

Db 910 ACCGATCAATTAAGCAGCAATATTTTCGTTCTGCTGCTACTATTTAGCTTATTTA 969

Qy 301 SerPheGlyTyr 304

Db 970 AGTTTCGATAT 981

RESULT 3

AY085036

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 1091)

Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.

Full-length messenger RNA sequences greatly improve genome annotation

Genome Biol. 3 (6), RESEARCH0029 (2002)

12093376

2 (bases 1 to 1091)

Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.

Full-length cDNA from Arabidopsis thaliana

Unpublished

3 (bases 1 to 1091)

Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.

Direct Submission

Submitted (11-MAR-2002) Ceres, Inc., 3007 Malibu Canyon Road, Malibu, CA 90265, USA

This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative

splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the We or later ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genes carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES

SOURCE

CDS

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REGRAEELKGPLFVIALFSAVFWRSEPIGMISSAMCGGSDINGMRKGSYK
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SLPTDLDNDVSVPLATITLAVISFGV"

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ORIGIN

Alignment Scores:

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Pred. No.:      1..46-127      Length:      1091
Score:          1523.00      Matches:      300
Percent Similarity: 99.7%      Conservative: 3
Best Local Similarity: 98.7%      Mismatches: 1
Query Match:     99.2%      Indels:      0
DB:              15          Gaps:      0

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US-10-634-548-2 (1-304) x AY085036 (1-1091)

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QY 1 MetAAlaATHrleuProleuSerProileanHhseGluLeuCyArgPheGlyAsnAsn 20
DB 108 ATGGACAGAACCTTACCTCTATCTCCATCATCATCGTGTGCGTTGGGAAACAC 167
QY 21 SerleuThrThrHLSaxPheCySerProGlyPheLeuIleSerSerProCyPheIle 40
DB 168 TCTTTGACGATCACCGGTTCTGTTCTCTGCTTCTGATTTCTTCTCTGTTTCAAT 227
QY 41 GlyLeuThrGlyMetGlySerAlaThrGlnLeuArgAlaArgSerLeuIleSerSer 60
DB 228 GGTTCGACCGGAATGGGCTCTGCTACTCATCGTTCGCTCTCTGATCTCTTCA 287
QY 61 AlaValAlaThrAsnSerLeuLeuHLSaPValGlyAlaThrValAlaValLeuGly 80
DB 288 GCAGTGGGAGAAATTCCTCTGTGATACGTCGAGCCACCGTGGCACTTGTGGA 347
QY 81 AlaTyrAlaLeuValIleuSerPheGlyuSerLeuThrIlySArGAsnValIleGlnGlnSer 100
DB 348 GCATACGCGCTTGTCTTAAGCTTCGAGAGTCTCACCAAGCAAGTCAATTCACAGAGT 407
QY 101 LeuSerArgIyLeuValHLSIleLeuSerGlyLeuLeuPheValLeuIleTrrProIle 120
DB 408 TTGAGCAGAAAGCTTGTGCATATCTCTCAGGTCGCTTTCGTACTTGCCTGGCCATTC 467
QY 121 PheSerGlySerThrGlyAlaArgTyrPheAlaAlaPheValProLeuValAsnGlyLeu 140
DB 468 TTCAGCGGATGACCGAGCTCGATATCTTTCGCTTTTGTTCGTTAGTAATGGCTTA 527
QY 141 ArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMetLeuIleIySerValThr 160
DB 528 AGCGTGTATTATTAAGCACTATCCATTTCCCAAAATTCGATGCTTAATAATCCGTCCA 587
QY 161 ArgTglIyArgAlaGluGlnLeuLeuIyGlyProLeuPheTyrValLeuAlaLeuLeu 180

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DB 588 AGGAAGGGGAGACAGAGAGTGTCTTAAGGCTCTTGTCTTACGTTACGCTTCTT 647
QY 181 PheSerAlaValPhePheTTPARGLuSerProIleGlyMetIleSerLeuAlaMetMet 200
DB 648 TTCTTCGCGGTTTCTTCTGAGAGATCTCTCATGCTGATGATCTGTTAGCAATATG 707
QY 201 CyGlyGlyAAspGlyIleAlaAspIleMetGlyArgIyAspPheGlySerThrIyIlePro 220
DB 708 TGTGTGGCGCATGGAATAGCTGATATATATGAGACGTAAAGTTGGGTCAATAGATACCT 767
QY 221 TyrAsnProArgIySerTTPAlaGlySerIleSerMetPheIlePheGlyPhePheIle 240
DB 768 TACAAACCAAGAAAGAGTTGGCAGAGAGCATCTCCATGTTCAATCTTCGCTCTTATC 827
QY 241 SerIleAlaLeuLeuTyrIyTyrSerSerLeuGlyTyrLeuHLSaMetAsnTrrGluThr 260
DB 828 TCCATTCGATTTACTTTACTTACTCTCAAGGCTTGGTACCTTCACTTAATCGGAAACG 887
QY 261 ThrLeuGlnArgValAlaMetValSerMetValAlaThrValAlaGluSerLeuProIle 280
DB 888 ACCTTGACAGAGATGACAAATAGTCTCAATGTAAGCCAGGTGGTCGAGTGCATCCATC 947
QY 281 ThrAspGlnLeuAspAspAsnIleSerValProLeuAlaThrIleLeuAlaAlaTyrLeu 300
DB 948 ACCGATCAATTAGACAGCAACGTTTGGTCTCTGCTACTATTTTAACCTGCTTATTTA 1007
QY 301 SerPheGlyTyr 304
DB 1008 AGTTTCGGAATTT 1019

RESULT 4
ATT32M21
LOCUS
DEFINITION
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project).
ACCESSION
AL162875.1 GI:7406444
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1 (bases 1 to 93045)
Bevan,M., Terry,N., Ardiles,W., Buyssehaert,C., Dasseville,R., De
Clerck,R., De Keyser,A., Neyt,P., Rouze,P., Van den Daele,H.,
Villareel,R., Gielen,J., Van Montagu,M., Bancroft,I., Mewes,H.W.,
Rudd,S., Lemcke,K. and Meyer,K.F.X.
Unpublished
2 (bases 1 to 93045)
EU Arabidopsis sequencing,project.
JOURNAL
TITLE
Submitted (31-MAR-2000) MIRP, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
lemcke@mipl.biochem.mpg.de, mayer@mipl.biochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbsrc.ac.uk
COMMENT
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
FEATURES
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1..1000
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676..3112
/gene="T32M21_10"
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gene

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WPCOMMENT

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DEFINITION complete sequence.
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VERSION AL606619.3 GI:32488370
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ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Euphorbiaceae; Oryzae; Oryza.
REFERENCE
AUTHORS
1. Feng, Q., Zhang, Y., Hao, P., Wang, S., Fu, G., Huang, Y., Li, Y., Zhu, J.,
Liu, Y., Hu, X., Jia, P., Zhang, Y., Zhao, Q., Ying, K., Yu, S., Tang, Y.,
Weng, Q., Zhang, L., Lu, Y., Mu, J., Lu, Y., Zhang, L. S., Yu, Z., Fan, D.,
Liu, X., Lu, T., Li, C., Wu, Y., Sun, T., Lei, H., Li, T., Hu, H., Guan, J.,
Wu, M., Zhang, R., Zhou, B., Chen, Z., Chen, L., Jin, Z., Wang, R.,
Yin, H., Cai, Z., Ren, S., Lv, G., Gu, W., Zhu, G., Tu, Y., Jia, J.,
Zhang, Y., Chen, J., Kang, H., Chen, X., Shao, C., Sun, Y., Hu, Q.,
Zhang, X., Zhang, W., Wang, L., Ding, C., Sheng, H., Gu, J., Chen, S.,
Ni, L., Zhu, P., Chen, W., Lan, L., Lai, Y., Cheng, Z., Gu, M., Jiang, J.,
Li, J., Hong, G., Xue, Y. and Han, B.
Sequence and analysis of rice chromosome 4
Nature 420 (6913), 316-320 (2002)
12447439
TITLE
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AUTHORS
2.
P. G., Wang, S. Y., Ren, S. X., Lv, G., Lin, W., Gu, W. Q., Zhu, G. F.,
Tu, Y. F., Jia, J., Yin, H. F., Zhang, Y., Cai, Z., Chen, J., Kang, H.,
Chen, X. Y., Shao, Y., Sun, Y., Hu, Q. P., Zhang, X. L., Zhang, W.,
Wang, L. J., Ding, C. W., Sheng, H. H., Gu, J. L., Chen, S. T., Ni, L.,
Zhu, F. H., Han, B., Feng, Q., Huang, Y. C., Li, Y., Zhu, J. J., Zhao, Q.,
Hu, X., Liu, Y. L., Wu, J., Yu, Z., Chen, L., Fan, D. L., Weng, Q. J.,
Zhang, L., Lu, Y. Q., Yu, S. L., Liu, X. H., Lu, T. T., Zhang, Y. J., Lu, Y.,
Li, C., Li, T., Zhang, Y., Hu, H., Jia, P. X., Qian, Y. M., Ying, K.,
Zhou, B., Chen, Z. H., Hao, P., Zhang, L., Wu, M., Zhang, R. Q., Guan, J. P.
and Hong, G. F.
Direct Submission
Submitted (08-SEP-2001) Han Bin, National Center for Gene Research,
Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233,
CHINA. E-mail enquiries: Dhanengr.ac.cn. Clone requests:
dhanengr.ac.cn
Oryza sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC
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On Jul 9, 2003 this sequence version replaced gi:21912468.
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JOURNAL Science 301 (5631), 376-379 (2003)
 PUBMED 12869764
 REFERENCE 2 (bases 1 to 1218)
 AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hirooka, T., Hori, P., Horita, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Maeda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohsuki, K., Oka, M., Ooka, H., Oshio, N., Oca, Y., Ootomo, Y., Ryu, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shikazume, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yanagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

TITLE Direct Submission
JOURNAL Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp).
 Tel:81-29-838-7007, Fax:81-29-838-7007

COMMENT This clone is one of the 28K full-length cDNA clones from japonica rice.

URL : http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_cDNA_Project_Team_Kikuchi_S_Satoh_K_Nagata_T_Kawagashira_N_Doi_K_Kishimoto_N_Yazaki_J_Ishikawa_M_Yamada_H_Ooka_H_Horita_I_Kojima_K_Namiki_T_Ohneda_E_Yanagi_W_Suzuki_K_Li_C_Ohsuki_K_Shishiki_T_Yamamoto_M

PLS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Maeda, H., Miura, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hirooka, T., Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ootomo, Y., Oshio, N., Oca, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shikazume, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

FEATURES
Source
 Location/Qualifiers

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 /cultiyar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="002-170-G04"

ORIGIN

Alignment Scores:

Pred. No.: 1..11e-38 **Length:** 1218
Score: 536.50 **Matches:** 123
Percent Similarity: 59.0% **Conservative:** 48
Best Local Similarity: 42.4% **Mismatches:** 100
Query Match: 34.9% **Indels:** 19

DB: US-10-634-548-2 (1-304) x AK110748 (1-1218)
DB: 15 **Gaps:** 8
Qy 18 GlysAsnAsnSerLeuThrThrHisArgPheCysSerProGlyPheLeuIleSerSerPro 37
Db 101 GGAATAATATCA-----AGTCACGACACCC-----TTAATACATACAGTA 142
Qy 38 CysPheIleGlyLeuThrGlyMetGlySerAlaThrGlnLeuArgAlaArgSerLeu 57
Db 143 TGTAAATCTGAGATTGTGTC-----CGCTCCGCTAGCAAGGCC 181
Qy 58 IleSerSerAlaValAlaThrAsnSerLeuLeuHisArgValGlyAlaThrValAlaVal 77
Db 182 TCATTCATGATGATTCGAGAGCCGCTGCGGAGACCGCGGCC-----GCCGTG 235
Qy 78 LeuGlyGlyAlaTyrrAlaLeu--ValLeuSerPhe--GluSerLeuThrIleArgAsn 95
Db 236 CTCACCGAGCCACCGCCCTCGCGCTTCGTTCTGGGAGAGCGTGGCAACCGCGCC 295
Qy 96 ValIleGlnGlnSerLeuSerArgIleValHisIleLeuSerGlyLeuLeuPheVal 115
Db 296 CTCCTTGACCAAGAACTCTGCAGAACTGTGCATTTACTGTGGCTTAGTACTTC 355
Qy 116 LeuAlaTrpProIlePheSerGly--SerThrGlnAlaArgTyrrPheAlaIlePheVal 134
Db 356 CTATATGCGCTTGTTCAGTGGAGATGATGATGATGATGATGATGATGATGATGATG 415
Qy 135 ProLeuValAsnGlyLeuArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMet 154
Db 416 ATTCATTCAACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 475
Qy 155 LeuIleYsSerValThrArgGlnGlyArgAlaGlnGlnLeuLeuYsGlyProLeuPhe 174
Db 476 GTCATTTACTCTTCATGACGAGAAACGAGACCGAGAGAGCTTTCTTAAGTCCACTGTAC 535
Qy 175 TyrValLeuAlaLeuLeuPheSerAlaValPhePheTrpArgGlnSerProIleGlyMet 194
Db 536 TAGCTGTGCTTAACACTCGCTACTGTAATTTCTGGAGGACATCTCCATTTCAATC 595
Qy 195 IleSerLeuAlaMetMetCysGlyGlyAspGlyIleLeuIleAsnIleMetGlyArgGlyPhe 214
Db 596 GCAAGTATTTGCAACTGTGTGCGGAGATGTGTACTCAATCAATGAGTGAAGCGCATTC 655
Qy 215 GlySerThrIleYsIleProIleArgAsnProArgIleSerTrpAlaGlySerIleSerMetPhe 234
Db 656 GGCATGTAATAGCTTCTCTTCAACCTCGATAGCTTATGCTGATTCATTCGCAATGTC 715
Qy 235 IlePheGlyPhePheIleSerIleAlaLeuLeuTyrrTyrrSerSerLeuGlyTyrrLeu 254
Db 716 TTAGCTGTTCCTTGTGCATCAATCTGTACATGCTACTGCTCCACTTGTGGATTTGTC 775
Qy 255 HisMetLeuTrpGlnTrpThrIleGlnAlaArgValAlaMetValSerMetValAlaThrVal 274
Db 776 GAGGAGAGCTGAGCATGTGATC--GCCTTGTGTGTCATCGCTGCTGCTGCAATY 832
Qy 275 ValGlnSerLeuProIleThrAspGlnLeuAspAspAsnIleSerValProLeuAlaThr 294
Db 833 GTGAGTCATCTCTTCTATCAGACACGCTGAGACACATCTGATGTGCCATGCGCTCT 892
Qy 295 IleLeuAlaAlaTyrrLeuSerPheGlyTyrr 304
Db 893 GTCTCTGTGTGTGCTGTGTTTCTATTAT 922

RESULT 10
AK176090 1211 bp **mRNA** linear **PLN** 09-SEP-2004
LOCUS Arabidopsis thaliana mRNA, complete cde, clone: RAF122-86-421.
ACCESSION AK176090
VERSION AK176090.1 GI:51970321
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1 Totoki, Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, N., Oishi, K., Kohara, Y., Kobayashi, M., Toyoda, A., Sakaki, Y., Sakurai, T., Iida, K., Akiyama, K., Satou, M., Toyoda, T., Konagaya, A., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K. Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs unpublished

2 (bases 1 to 1211)

3 Totoki, Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, N., Oishi, K., Kohara, Y., Kobayashi, M., Toyoda, A., Sakaki, Y., Sakurai, T., Iida, K., Akiyama, K., Satou, M., Toyoda, T., Konagaya, A., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K. Direct Submission

4 Submitted (06-SEP-2004) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: maseki@gsc.riken.jp, URL: http://large-gsc.riken.jp/, Tel: 81-45-503-9625, Fax: 81-45-503-9586)

5 An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda phage-1-E vector (Carninci et al. (2001) Genomes 77:79-90) digested with BamHI and SalI. This clone is in a modified pBlueScript vector. Please visit our web site (http://large-gsc.riken.jp/) for further details.

FEATURES

source location/Qualifiers

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CDS 5..928 /gene="At5g58560"

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ORIGIN

Alignment Scores:

pred. No.: 3.11e-38 Length: 1211

Score: 531.50 Matches: 120

Percent Similarity: 59.0% Conservative: 66

Best Local Similarity: 38.1% Mismatches: 108

Query Match: 34.6% Indels: 21

DB: 15 Gaps: 7

US-10-634-548-2 (1-304) x AK176090 (1-1211)

QY 1 MetAlaAlaThrLeuProLeuSerProIleAsnHISGLInLeuCyArGpHeGlyAsnAsn 20

DB 5 ATGGCACTACTGTACTACTACAAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 64

QY 21 SerLeuThrThrIstArgPheCySerPro-----GlyPheLeuIleSerSerPro 37

DB 65 CCTCTCTGTGAC-----TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCGATTCCA 112

QY 38 CyPheIleGlyLeu-----ThrGlyMetGlySerAlaThrGlnLeuArgAlaArg 54

DB 113 CGATTCTCACTGCTCGAATCGGACCTGTTAGATGAGCTCTGAGTTTCCGGCCACC 172

QY 55 ArgSerLeuIleSerSerAlaValAlaThr-----AsnSerLeuLeuHisAsp 70

DB 173 AATATCCGAGCTTTCACCTCGCGCGCGGTGATGTTCCGGAATTCGGTTTATCATGAT 232

QY 71 Val-----GlyAlaThrValAlaValLeuGlyGlyAlaTyrAlaValLeuSer 87

DB 233 GTCGCGCGTTCGAGTCACTGACCTGATGTT-----GCGTTCCTGCTCCGCGTTTC 283

QY 88 PheGluSerLeuThrIstArgAsnValIleGlnGlnSerLeuSerArgGlyLeuValHis 107

DB 284 TGGGAGAGATTGGCAACCTGGCACTTTCGACCAAGAACTCATCCGGAAGCTTGTCAT 343

QY 108 IleLeuSerGlyLeuLeuPheValLeuAlaTyrProIlePheSerGlySerThrGluAla 127

DB 344 ATAAATATTGGCTAGATTATTTATGCTTGTGCGCGCTGTTGATGTTGGAATCCAGGA 403

QY 128 ArgTyrPheAlaAlaPheValProLeuValAsnGlyLeuArgLeuValIleAsnGlyLeu 147

DB 404 GCATTTTCGATCTCTTGTACCTGACCTCAATATAGTAAAGATGATGCTGCGGCTT 463

QY 148 SerIleSerProAsnSerMetLeuIleValSerValThrArgGluGlyArgAlaGlu 167

DB 464 GAGATGACACAGACGAGGAGAACATCAATGATGATGACGACATGAGATTCGAGGAA 523

QY 168 LeuLeuIleGlyProLeuPheTyrValLeuAlaLeuLeuPheSerAlaValPhePheTyr 187

DB 524 CTACTTAAGGGCGCGCTTATCTATGTACTGATCATCATCATCATCCGCTCTACTATGG 583

QY 188 ArgGluSerProIleGlyMetIleSerLeuAlaMetMetCysGlyGlyAspGlyIleAla 207

DB 584 AATATCATCCCAATCGGATTCGGATTCGGATTCGATTCGATTCGATTCGATTCGATTC 643

QY 208 AsnIleMetGlyArgGlyPheGlySerThrValIleProTyrTrpAsnProArgGlySerTyr 227

DB 644 GACATTTGGTGGGCGGTTTGAACAGAGAACTTCTTCAACAAACAAATCATTTT 703

QY 228 AlaGlySerIleSerMetPheIlePheGlyPhePheIleSerIleAlaLeuLeuTyrTyr 247

DB 704 GCTGTAGCATTTGGATGCGCACCGCGGCTTCTAGCATCTGTTGGTATGATGATCTAC 763

QY 248 TyrSerSerLeuGlyTyrIleuHisMetAsnTyrGluThrThrLeuArgValAlaMet 267

DB 764 TTGCTTCAATTTGTTATCATCGAGATGAGCGGGGAATGATTCCTT---CGTTCTCTGTC 820

QY 268 ValSerMetValAlaThrValValGluSerLeuProIleThrArgGlnLeuAspAspAsn 287

DB 821 ATCTCATAGCATCACTCTTGGATGATCTCTCCCAATTAAGACCAATTCATTCGACAAAT 880

QY 288 IleSerValProLeuAlaThrIleLeuAlaAlaTyrIleSerPhe 302

DB 881 CTCACATTTCTTAACTCTGCTTGGCGGATTCCTACTCTTC 925

RESULT 11

AK176217

LOCUS 1360 bp mRNA linear PLN 09-SEP-2004

DEFINITION Arabidopsis thaliana mRNA, complete cds, clone: RAF123-09-006.

ACCESSION AK176217

VERSION AK176217.1 GI:51970575

KEYWORDS FLI cDNA.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1 Totoki, Y., Seki, M., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Shin-i, T., Nakagawa, M., Sakamoto, N., Oishi, K., Kohara, Y., Kobayashi, M., Toyoda, A., Sakaki, Y., Sakurai, T., Iida, K.,

JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1162)
 AUTHORS Brover, V., Trounhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
 TITLE Direct Submission
 JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA

COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made available to RIKR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants; including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the M8 or M9 ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genes carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES
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 TIKMSRHGRRELKGPLYVLSITSACTYKSSPIALAVICNLGAGGMADIVR
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 SALVESLPISTIDIDNTLITSLAAGFLF"

ORIGIN
 Alignment Scores:
 Pred. No.: 8,32e-38 Length: 1162
 Score: 526.50 Matches: 118
 Percent Similarity: 58.7% Conservative: 67
 Best Local Similarity: 37.5% Mismatches: 109
 Query Match: 34.3% Indels: 21
 DB: 15 Gaps: 7

US-10-634-548-2 (1-304) x AY087555 (1-1162)

QY 1 MetAlaAaThrLeuProLeuSerProIleAsnHleGlnLeuCyAArgPheGlyAsnAsn 20
 Db 23 ATGGCAACTACTACTACTACCAAGAGCTCCGCTTCCTGCTCTTCAATTCATCT 82
 QY 21 SerLeuThrThrHleArgPheCySerPro-----GlyPheLeuIleSerSerPro 37
 Db 83 CCTCTCTGTTGAC-----TCTCTCTCTCTCTCTCGCTTCTTCTCCGATTCCA 130
 QY 38 CyAheIleGlyLeu-----ThrGlyMetGlySerAlaThrGlnLeuArgAlaArg 54
 Db 131 CGATTCTCTGACTGTCGCAATCGCACTTAGATGACCTTAGAGTTTCCGACACC 190
 QY 55 ArgSerLeuIleSerSerAlaValAlaThr-----AanSerLeuLeuHleAsp 70
 Db 191 AAATATCGCAAGCTTCTACCTCGCGCCGTGATGTTCCGAAATTCGCTTTATCAAT 250
 QY 71 Val-----GlyAlaThrValAlaValLeuGlyAlaTyrAlaLeuValLeuSer 87
 Db 251 GTCTGCGGCTTTGGAGTCACTAGCATCGTT-----CGCTTCTCGTCCGCTTC 301
 QY 88 PheGluSerLeuThrIlyArgAsnValIleGlnGlnSerLeuSerArgIlyLeuValHis 107

Db 302 TGGGAGAGAGATGGCAAAAGCTGGCATCTTGACACCAAGAACTCATCCGGAAGCTTGAT 361
 QY 108 ILeuSerGlyLeuLeuPheValLeuAlaTyrProIlePheSerGlySerThrGluAla 127
 Db 362 ATAAATATGGGAGTAAAGTTTATGCTTTCCTGGCGCGCTGTTCACTGCAATCCAGGA 421
 QY 128 ArgTyrPheAlaAlaPheValProLeuValAsnGlyLeuArgLeuValIleAsnGlyLeu 147
 Db 422 GCACCTTTCGATCTCTTGAACCTGCACTCAATATATTAAGATGATTCGCGGCTT 481
 QY 148 SerIleSerProAsnSerMetLeuIleYleSerValThrArgGluIlyArgAlaGluGlu 167
 Db 482 GAGATGATACCAAGCAAGAGAAATCAATGATGATGAGACATGAGATCCGAGGGA 541
 QY 168 LeuLeuGlyGlyProLeuPheTyrValLeuAlaLeuLeuPheSerAlaValPhePheTyr 187
 Db 542 CTACTTAAAGGGGCGCTTCTTACTAGTACTGTCATCATCATCAGCTCATCTACTATTGG 601
 QY 188 ArgGluSerProIleGlyMetIleSerLeuAlaMetMetCyGlyGlyAspGlyTyrAla 207
 Db 602 AAATCATCCCGATCCGATGCGGATGCGGTATGACACCTTGGCGAGAGATGATGGCT 661
 QY 208 AspIleMetGlyArgIlyPheGlySerThrIlySileProIlyAsnProArgIlySerTyr 227
 Db 662 GACATTTGGGTGGCGCGCTTGGACACAGAGAGCTTCTTACAAACAAATCATTT 721
 QY 228 AlaGlySerIleSerMetPheIlePheGlyPhePheIleSerIleAlaLeuLeuTyrTyr 247
 Db 722 GCTGTAGCATTTGGAATGGCCACCGCGGTTTCTACATCTGTTATATATCTACTAC 781
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 Db 839 ATCTCTATAGCATAGAGCTCTTGTGATCACTCCCAATAGACACCGCATTTGAGACAT 898
 QY 288 ILeSerValProLeuAlaThrIleLeuAlaTyrLeuSerPhe 302
 Db 899 CTCACATTCCTTACCTCTGCGCTTGGCGGATCTTACTCTTC 943

RESULT 13
 AK065924/c 3143 bp mRNA linear PLN 24-JUL-2003
 LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:J013046L2, full
 DEFINITION insert sequence.
 ACCESSION AK065924
 VERSION AK065924.1 GI:32975942
 KEYWORDS Full_cDNA; CAP trapper.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriatroidae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS 1 The Rice Full-length cDNA Consortium, National Institute of
 Agrobiological Sciences Rice Full-length cDNA Project Team;
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Oike, H., Hotta, I.,
 Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
 Onitsuki, K., Shishiki, T., Foundation of Advancement of International
 Science Genome Sequencing & Analysis Group; Otono, Y., Murakami, K.,
 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tamoda, Y.,
 Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
 Marikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J.,
 Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
 Kusumegi, T., Oka, M., Ryu, K., Ueda, M., Matsubara, K., RIKEN;
 Kawai, J., Carinanci, P., Adachi, J., Aizawa, K., Arikawa, T., Fukuda, S.,
 Hara, A., Hashidume, M., Hayatsu, N., Imocant, K., Ishii, Y., Itoh, M.,
 Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Oeato, N., Oca, Y.,
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TITLE	Yoshino, M. and Hayashizaki, Y. Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice Science 301 (5631), 376-379 (2003)		
JOURNAL	12869764		
REFERENCE	2 (bases 1 to 3143)		
AUTHORS	Adachi, J., Alzawa, K., Akimura, T., Arahawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamura, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Naitoki, T., Naitaka, R., Naitaka, J., Nishii, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Oosato, N., Ota, Y., Otsu, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yanagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.		
TITLE	Direct Submession		
JOURNAL	Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: shikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)		
COMMENT	This clone is one of the 28K full-length cDNA clones from japonica rice. URL : http://cdna01.dna.affrc.go.jp/cDNA/ NIAS_Rice_Full-length_cDNA_Project_Team_Kikuchi_S.,Satoch_K., Nagata_T.,Kawagashira_N.,Doi_K.,Kishimoto_N.,Yazaki_J., Ishikawa_M.,Yamada_H.,Ooka_H.,Hotta_I.,Kojima_K.,Naitoki_T., Ohneda_E.,Yanagi_W.,Suzuki_K.,Li_C.,Ohtsuki_K.,Shishiki_T. and Yamamoto_M.		
FEATURES	RAIS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamura, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Naitaka, R., Naitaka, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken: Adachi, J., Alzawa, K., Akimura, T., Arahawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishii, K., Nomura, K., Numasaki, R., Ohno, M., Oosato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y. Location/Qualifiers 1. .3143 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultiivar="Nipponbare" /db_xref="taxon:39947" /clone="J013046L12"		
ORIGIN			
Alignment Scores:			
Pred. No. :	3.03e-37	Length:	3143
Score:	526.50	Matches:	126

Percent Similarity:	50.1%	Conservative:	43
Best Local Similarity:	37.4%	Mismatches:	37
Query Match:	34.3%	Indels:	133
DB:	15	Gaps:	4
US-10-634-548-2 (1-304) x AK065924 (1-3143)			
Qy 99 GlnSerLeuSerArgIysLeuValHisIleLeuSerGlyLeuLeuPheValIleAlaTyr 118			
Db 2920 CAGAGCTGAGCAGAAAAATTGGCATGTGCTCTCCGAGAGTCTGTTCATGTCTTCTGG 2861			
Qy 119 ProlIlePhe----- 121			
Db 2860 CCACTATTCAGGTCCTCCCTTCCCACTGCTCTTCCAGATCGAAAGTTTCTTCAACCA 2801			
Qy 122 -----SerGlySerThrGluAlaAr 128			
Db 2800 AATCAGACTAGAGATCTTAAGAAATATGATGCCCTTCCGAGTAATTCAGACAGACAGC 2741			
Qy 128 GTYrPheAlaIlePheValProLeuValAangIysLeuValIleangIysLeu 148			
Db 2740 GTTCTTCGCGCAATTGTCCTGTTGCTGAATCGATAGAGCTTCTGACCTACGCGCTCCG 2681			
Qy 148 rIleSerProAnsSerMetLeuIleIysSerValThrArgGluGlyArgAlaGlu----- 166			
Db 2680 CTTTTCACATGATGAAGCTCTAGTAATCGTGACCCGTAAGAGAAACCAAGATTTCGT 2621			
Qy 166 ----- 166			
Db 2620 GCTATGATCTCTTATTTCTGATCTCTTCAATCAAAAATGATATTCCTTGACAT 2561			
Qy 167 -----GluLeuLeuIysGlyProLeuPheTyValLeuAlaLeuL 180			
Db 2560 GATCTTGTGTTGCTTACAGGAAATGCTGAGAGGTCCTGTAATGATGATGTGCTGC 2501			
Qy 180 eupheserAlaValPhePheThrArgIysSerProIleGlyMetIleSerLeuAlaMetM 200			
Db 2500 TGGTCACTGTTTGGTCTTCTTGGCGCAGTCTCTATGGAAATGTTGTTGTTGCGATGA 2441			
Qy 200 eCyGslGlyIAspGlyIle----- 206			
Db 2440 TGAAGTGTGATGATGTA-GATGTTGATCTCTCGGAATTTAGAGAAATTCGACATT 2382			
Qy 206 ----- 206			
Db 2381 TTTTGTATATACCCAGTTCACTGATGAATGATCTTCTGCTAGTATATCCACT 2322			
Qy 207 -----AlaAspIleMetGlyArgGlyPheGlySerThrL 218			
Db 2321 TCTTGTCTTATTTTTCAGGCTTGTGCTGATGTTGGAGAGATAGGCTCCGCGA 2262			
Qy 218 yslIleProTyAsnProArgIysSerTrpAlaGlySerIleSerMetPheIlePheGlyP 238			
Db 2261 AGCTGCCATTCATGAGAACAGACAGCTGATAGGAAACATCTCAATTCTTCTGGCT 2202			
Qy 238 hepheIleSerIleAla----- 243			
Db 2201 TCCTTTATCTGCG-ACGTAGAGTTTTCCTTCAGATGATGATGCTGCTTCTTTCATATG 2143			
Qy 244 -----LeuLeuTyTrpTyrS 249			
Db 2142 TTAATCTTGTATTTGTTAACTCATGATCTTTGATCATCAGAGATGCTTCTACTTCT 2083			
Qy 249 erSerLeuGlyTyLeuHisMetAsnTrpGluThrThrLeuGluAlaValAlaMetValS 269			
Db 2082 CTTCGCTTGTGTTACTTACATGTCGTGCGATGCGACATTCGTAATCTGCTTGTGTG 2023			
Qy 269 erMetValAlaThrValValGluSerLeuProIleThrAspGlnLeuAspAspAsnIleS 289			
Db 2022 CATTAAGCACTACTAGTGAAGTATGATCTCTGTCATGATGTTGTGATGACAAATATCT 1963			
Qy 289 erValProLeuAlaThrIleLeuAlaIleTyIleuSerPheGlyTyTr 304			

Db 1962 CCGTTCCTTGCCACCATGTTGGAGCGCTAATCTGTATTATTGGCTAC 1916

RESULT 14

AKI09049 1059 bp mRNA linear PLN 24-JUL-2003

LOCUS AKI09049

DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:002-154-B02, full insert sequence.

VERSION AKI09049

KEYWORDS AKI09049.1 GI:32994258

ORGANISM Pfl_CDNA; oligo capping.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euhartoideae; Oryzaceae; Oryza.

REFERENCE 1

THE RICE FULL-LENGTH CDNA CONSORTIUM, National Institute of Agricultural Sciences Rice Full-Length cDNA Project Team; Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Nemiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Oono, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurotski, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Naitaka, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN; Kawai, J., Carninci, P., Adachi, J., Atzawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Oono, N., Oca, Y., Sato, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

Science 301 (5631), 376-379 (2003)

JOURNAL PUBMED 12869764

REFERENCE 2 (bases 1 to 1059)

ADACHI, J., ATZAWA, K., AKIMURA, T., ARAKAWA, T., CARNINCI, P., DOI, K., FUJIMURA, T., FUKUDA, S., HANAGAKI, T., HARA, A., HASHIDUME, W., HAYASHIZAKI, K., HAYASHIZAKI, Y., HAYATSU, N., HIMOTO, K., HIROKA, T., HORI, F., HOTTA, I., IIDA, J., IIDA, Y., IKEDA, R., IMAMURA, K., IMOTANI, K., ISHIBIKI, J., ISHII, Y., ISHIKAWA, M., ITOH, M., KAGAWA, I., KANAGAWA, S., KATO, H., KAWAGASHIRA, N., KAWAI, J., KAWAMATA, M., KIKUCHI, S., KISHIKAWA-HIROKAWA, T., KISHIMOTO, N., KOBAYASHI, M., KODAMA, T., KOJIMA, K., KOJIMA, Y., KONDO, S., KONNO, H., KONDA, M., KOYA, S., KURIHARA, C., KUROSAKI, T., KUSUMEGI, T., LI, C., LU, M., MASUDA, H., MATSUBARA, K., MATSUYAMA, T., MIURA, C., MIYAZAKI, A., MIZUNO, K., MURAKAMI, K., MURATA, M., NAGATA, T., NAKAMURA, M., NAMIKI, T., NAITAKAWA, R., NIKIURA, J., NISHII, K., NOMURA, K., NUMASAKI, R., OHNEDA, E., OHNO, M., OHTSUKI, K., OKA, M., OKA, H., OONO, N., OCA, Y., OONO, Y., RYU, R., SATOH, H., SAKAI, C., SAKAI, K., SAKAZUME, N., SANO, H., SASAKI, D., SATO, K., SATOH, K., SHIBATA, K., SHINAGAWA, A., SHIRAKI, T., SHISHIKI, T., SOGODE, Y., SUGANO, S., SUGIYAMA, A., SUZUKI, K., SUZUKI, Y., TAGAMI, M., TAGAMI-TAKEDA, Y., TAGAWA, A., TAKAHASHI, F., TAKEKUNI-KHARA, S., TANAKA, T., TOMARU, A., TOYA, T., TSUNODA, Y., UEDA, M., WAKI, K., XIE, Q., YAHAGI, W., YAMADA, H., YAMAMOTO, M., YASUNISHI, A., YAZAKI, J., YOKOMIZO, S., and YOSHIMURA, A.

Direct Submission

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp; Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28k full-length cDNA clones from japonica rice.

URL : http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_cDNA_Project_Team_Kikuchi_S.,_Satoh_K.,_Nagata_T.,_Kawagashira_N.,_Doi_K.,_Kishimoto_N.,_Yasaki_J.,_Ishikawa_M.,_Yamada_H.,_Ooka_H.,_Hotta_I.,_Ishikawa_M.,_Yamada_H.,_Ooka_H.,_Hotta_I.,_Kojima_K.,_Nemiki_T.,_Ohneda_E.,_Yahagi_W.,_Suzuki_K.,_Li_C.,_Ohtsuki_K.,_Shishiki_T.,_and_Yamamoto_M.

COMMENT


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Db      10016  TACGCGGCGACGTTGCGG---ATCTCGTGGCGCGTGGCGTTGTGGAATGCTCCGGTC 99960
Qy      281  ThrAepGlnLeuAepAepAenIIeSerValProLeuAlaThrIIeLeuAlaAlaTyrLeu 300
      ::: ||||| ||||| ||||| |||||
Db      99959  TCATCCGCTCTTGAAGACAACTTCACCGCTGCTTTCACCGCGTGGCGTGGGAACGTTG 99900
Qy      301  SerpHe 302
      |||
Db      99899  TTATTC 99894
  
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Search completed: March 16, 2006, 22:17:27
 Job time : 7927 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: March 16, 2006, 19:53:40 ; Search time 681 Seconds

(without alignments) 2975.134 Million cell updates/sec

Title: US-10-634-548-2

Sequence: 1 MATRLPLSPINHQLCRGN.....DDNISVPLATITLAAYLSFGY 304

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

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-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: geneseqn2001as:.*
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12: geneseqn2004as:.*
13: geneseqn2004bs:.*
14: geneseqn2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1536	100.0	1015	13	ADx46288
2	1536	100.0	1091	12	ADJ98163
3	1523	99.2	980	13	ADx31786
4	1523	99.2	1088	3	AAC36634

5	1284.5	83.6	1897	12	ADJ98165	AdJ98165 Thale cre
6	1266	82.4	1062	13	ADx54389	Adx54389 plant ful
7	870	56.6	1007	13	ADx45670	Adx45670 plant ful
8	794	51.7	1085	13	ADx47586	Adx47586 plant ful
9	788	51.3	1033	13	ADx51853	Adx51853 plant ful
10	776	50.5	798	13	ADx48515	Adx48515 plant ful
11	773	50.3	976	13	ADx51811	Adx51811 plant ful
12	751	48.9	723	13	ADx50931	Adx50931 plant ful
13	751	48.9	753	13	ADx51758	Adx51758 plant ful
14	742	48.3	937	13	ADx51714	Adx51714 plant ful
15	648	42.2	494	3	AAC53042	Aac53042 Zea mays
16	646	42.1	674	13	ADx34057	Adx34057 plant ful
17	573	37.3	916	13	ADx17675	Adx17675 plant ful
18	572.5	37.3	1225	13	ADx51722	Adx51722 plant ful
19	567.5	36.9	688	13	ADx47647	Adx47647 plant ful
20	566.5	36.9	666	13	ADx10350	Adx10350 plant ful
21	552.5	36.0	1091	13	ADx51558	Adx51558 plant ful
22	545.5	35.5	1241	13	ADx19540	Adx19540 plant ful
23	540.5	35.2	795	13	ADx30592	Adx30592 plant ful
24	539	35.1	867	13	ADx50633	Adx50633 plant ful
25	536.5	34.9	1046	13	ADx36475	Adx36475 plant ful
26	530.5	34.5	1160	3	AAC45477	Aac45477 Arabidops
27	530.5	34.5	1162	12	ADJ98167	AdJ98167 Thale cre
28	517	33.7	1193	13	ADx15971	Adx15971 plant ful
29	515	33.5	963	3	AAC46147	Aac46147 Arabidops
30	512	33.3	1029	13	ADx32079	Adx32079 plant ful
31	511.5	33.3	648	13	ADx34109	Adx34109 plant ful
32	509	33.1	944	13	ADx37159	Adx37159 plant ful
33	509	33.1	1106	13	ADx54040	Adx54040 plant ful
34	508	33.1	948	13	ADx37160	Adx37160 plant ful
35	492	32.0	1165	3	AAC40207	Aac40207 Arabidops
36	490	31.9	1044	13	ADx51812	Adx51812 plant ful
37	481.5	31.3	699	13	ADx50711	Adx50711 plant ful
38	479.5	31.2	793	13	ADx47651	Adx47651 plant ful
39	466	30.3	545	13	ADx45744	Adx45744 plant ful
40	440	28.6	1502	13	ADx34329	Adx34329 plant ful
41	430.5	28.0	1502	13	ADx45999	Adx45999 plant ful
42	392.5	25.6	776	13	ADx63685	Adx63685 plant ful
43	381.5	24.8	729	13	ADx60081	Adx60081 plant ful
44	366.5	23.9	631	13	ADx49148	Adx49148 plant ful
45	353	23.0	485	5	AAH87900	Aah87900 Pepermin

ALIGNMENTS

RESULT 1	ADx46288	standard; cDNA; 1015 BP.
ID	ADx46288	
XX	ADx46288;	
AC	ADx46288;	
XX		
DT	21-APR-2005	(first entry)
XX		
DE	Plant full length insert polynucleotide seqid 21028.	
XX		
KW	plant protectant; plant growth regulator; gene therapy; plant;	
KW	recombinant DNA construct; physical array; plant breeding marker;	
KW	cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;	
KW	extreme osmotic condition; pathogen tolerance; pest tolerance;	
KW	growth rate; cell cycle pathway; disease resistance;	
KW	glactomannan production; lignin production; plant growth regulator;	
KW	yield; plant growth; plant development; seed oil; protein yield;	
XX	protein content; gene; ss.	
XX		
OS	Unidentified.	
XX		
PN	US2004034888-A1.	
XX		
PD	19-FEB-2004.	
XX		
PF	28-APR-2003; 2003US-00425114.	
XX		
PR	06-MAY-1999; 99US-00304517.	

PR 05-NOV-2001; 2001US-00985678.

XX (LIU/) LIU J.

PA (ZHOU/) ZHOU Y.

PA (KOVA/) KOVALIC D K.

PA (SCRE/) SCREEN S E.

PA (TABAS/) TABASKA J E.

XX (CAOV/) CAO Y.

PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y, WPI; 2004-180133/17.

DR

XX New recombinant DNA construct, useful for improving plant tolerance to PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or PT pests, for conferring increased resistance to plant disease, or for PT improving yield.

XX

PS Claim 1; SEQ ID NO 21028; 15pp; English.

XX

CC The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?docid:200403488. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the invention.

CC

XX

SO Sequence 1015 BP; 228 A; 245 C; 219 G; 323 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Mismatches:	Indels:	Gaps:
Score: 1536.00	1015	304	0	0	0
Percent Similarity: 100.0%					
Best Local Similarity: 100.0%					
Query Match: 100.0%					

DB: 13

US-10-634-548-2 (1-304) x ADX46288 (1-1015)

QY 1 MetAlaAlaThrLeuProLeuSerProLeuAlaGlnLeuCyArgPheGlyAsnAsn 20

DB 35 ATGGGAGAACCTTAACCTTAATCTCCGATCAATCTGATGTCGATGCGGAGAACAC 94

QY 21 SerLeuThrThrAlaArgPheCySerSerProGlyPheLeuIleSerSerProCyPheIle 40

DB 95 TCTTGAAGCACTCAACGGTTCGTTCTCTGGCTTCTGATTTCTTCTCTGTTTCAATT 154

QY 41 GlyLeuThrGlyMetGlySerAlaThrGlnLeuArgAlaArgGlySerLeuIleSerSer 60

DB 155 GGTTCGACCGGAATCGGCTCTGCTACTCACTTACCTGCTCTCTCTATCTCTTCA 214

QY 61 AlaValAlaThrAsnSerLeuLeuHisAspValGlyAlaThrValAlaValLeuGlyGly 80

DB 215 GCAGTTGGAGCAAAATTCGCTGTGCATACGTCGAGCACCGTGGCAGTCTGGTGA 274

QY 81 AlaTyrAlaLeuValIleuSerPheGlySerLeuThrIleArgAsnValIleGlnGlnSer 100

DB 275 GCATACGGCTTGTCTTAAGCTTCAGAGTCTCACCAAGCGAAAGCTCATTCACAGAGT 334

QY 101 LeuSerArgGlyLeuValHisIleLeuSerGlyLeuLeuPheValLeuAlaTyrProIle 120

DB 335 TTGAGCAGAAAGCTTGTCATATATCTCTCAGCTTCGCTTTTCTGTACTCGCTGGCCATC 394

QY 121 PheSerGlySerThrGlnAlaArgTyrPheAlaAlaPheValProLeuValAsnGlyLeu 140

DB 395 TTCAAGCGGATCGAACCGAGGCTCGATCTTGTCTTGTTCGTTAGTGAAGGCTTA 454

QY 141 ArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMetLeuIleValSerValThr 160

DB 455 AGGCTGTATTTAAACGAGATATCATTTCCCAAAATTCGATGATCAATCAATCCGTACA 514

QY 161 ArgGlyGlyValArgAlaGlyGlyLeuLeuGlyGlyProLeuPheTyrValIleAlaLeuLeu 180

DB 515 AGAAGAGGAGAGAGAGAGAGAGTGTAAAGTCTTGTGTCTAGCTTCTTCTTCTT 574

QY 181 PheSerAlaValPhePheTyrArgGlySerProIleGlyMetIleSerLeuAlaMetMet 200

DB 575 TTCTCTCGGTTTCTTCTTCTGAGAGAGTCTCTATCGGTATGATCTGTTAGCATATAG 634

QY 201 CyAGlyGlyAspGlyIleAlaAspIleMetGlyArgGlyPheGlySerThrIlePro 220

DB 635 TGTGTGGCGATGGAAATAGCTGATATATAGGACGTAAAGTTGGGTCAACTTAAGATACCT 694

QY 221 TyrAsnProArgGlySerTyrPheAlaGlySerIleSerMetPheIlePheGlyPhePheIle 240

DB 695 TACAACCCAAAGAAAGAGTGGCGAGAGATCTCCATGTCATCTTCGCTTCTTCAATC 754

QY 241 SerIleAlaLeuLeuTyrTyrTyrSerSerLeuGlyTyrLeuHisMetAsnTyrGluThr 260

DB 755 TCCATGCCATTAATCTTACTTACTTACTCAAGCTTGGGATACCTTCAACGATCGGAAACG 814

QY 261 ThrLeuGlnArgValAlaMetValSerMetValAlaThrValValGlySerLeuProIle 280

DB 815 ACCTTGAGAGAGAGAGCAATGCTCAATGTCGCCACGAGTACGAGTCCGTACCAATC 874

QY 281 ThrAspGlnLeuAspAspAsnIleSerValProLeuAlaThrIleAlaAlaTyrLeu 300

DB 875 ACCGATCAATTAAGCGCAAAATTTCCGTTCTCTGCTACTATTTTAACTGCTTAATTA 934

QY 301 SerPheGlyTyr 304

DB 935 AGTTTCGATTAAT 946

RESULT 2

ADJ98163

ID ADJ98163 standard; DNA; 1091 BP.

XX

AC ADJ98163;

XX

XX 06-MAY-2004 (first entry)

XX

XX Thale cress LTT1 phycol kinase wild-type DNA.

XX

XX phycol kinase; tocopherol biosynthesis; plant; drought resistance; LTT1;

XX thale cress; ds; gene; wild-type.

XX

XX Arabidopsis thaliana.

XX

XX MO200401312-A2.

XX

PD 12-FEB-2004.

XX

XX 05-AUG-2003; 2003WO-US025276.

XX

XX 05-AUG-2002; 2002US-0400689P.

PR 05-AUG-2003; 2003US-00634548.

XX

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX

XX Norris SR, Lincoln K, Abad MS, Ellere R, Harteuylker KK;

PI Hirschberg J, Karunanandaa B, Moshiri F, Stein JC, Valentin HB;

PI Venkatesh TV;

XX

XX WPI; 2004-157125/15.

DR P-PSDB; ADJ98164.
 XX New phyto. kinase polynucleotides, useful in mediating tocopherol
 PT biosynthesis and in producing plants with increased drought resistance.
 XX
 PS Claim 4; SEQ ID NO 1; 189pp; English.
 XX
 CC The invention relates to a novel substantially purified nucleic acid
 CC molecule encoding a phyto. kinase. The nucleic acid molecules and
 CC polypeptides of the invention may be useful in mediating tocopherol
 CC biosynthesis and in producing plants with increased drought resistance.
 CC The current sequence is that of the chate cross LMT1 phyto. kinase wild-
 CC type DNA of the invention.
 XX
 XX Sequence 1091 BP; 252 A; 260 C; 223 G; 356 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,09e-165 Length: 1091
 Score: 1536.00 Matches: 304
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 12 Gaps: 0
 US-10-634-548-2 (1-304) x ADJ98163 (1-1091)
 QY 1 MetAlaIaIeUeuTYTYrSerSerLeuGlyTyrLeuHisMetAenTrpGluThr 20
 DB 108 ATGGACACCACTTACCTTATCTCCATCATATCATCGTTGTGCGTTCGGGAAACAC 167
 QY 21 SerLeuThrThriSarPheCySerProGlyPheLeuHisSerSerProCyPheIle 40
 DB 168 TCTTTGACGACTCACCGGTTCTGTCCTGCTTCTTGAATTTCTTCTCTTTTCAATT 227
 QY 41 GlyLeuThrGlyMetGlySerAlaThrGlnLeuAlaArgArgSerLeuHisSerSer 60
 DB 228 GGTGGACCGGAAGGGCTGCTGACTACGTTACGTTGCTGCTGCTGCTGCTGCTTCA 287
 QY 61 AlaValAlaThrAnSerLeuLeuHisAlaValAlaValAlaValAlaValAlaValGly 80
 DB 288 GCAGTTCGACGAAATGCTGTTGCAATGACGAGCCACCGGCGGACGTCGTTGGTGA 347
 QY 81 AlaTyrAlaLeuValLeuSerPheGlySerLeuThriLysArgAenValIleGlnGlnSer 100
 DB 348 GCATACCGCTGCTGCTTATGCTTCAAGTCTCCACAGGAAACGTCATTCAACAGAGT 407
 QY 101 LeuSerArgLysLeuValHisIleLeuSerGlyLeuLeuPheValAlaTrpProIle 120
 DB 408 TTGAGCAGAAAGCTTGATGATATATCTCAGGTCGCTTTTCGTAATTCGTCGCAATC 467
 QY 121 PheSerGlySerThriGlnAlaArgTyrPheAlaAlaPheValProlLeuValAenGlyLeu 140
 DB 468 TTCAGCGAATCGACGAGGCTCGAATCTTGTCTTGTTCGTTAGTAAGGCTTCA 527
 QY 141 ArgLeuValIleAenGlyLeuSerIleSerProAnSerMetLeuIleLysSerValThr 160
 DB 528 AGCGTTGTTATTAACGAGACTATTCATTTCCCAATTCGATGCTAAATCAATCCGTCACA 587
 QY 161 ArgGlnGlyArgAlaGlnGlnLeuLeuLysGlyProlLeuPheTyrValLeuAlaLeuLeu 180
 DB 588 AGAGAAAGGAGAGAGAGAAAGATTCCTTAAGGTCCTTGTGTTCTTCAAGTTCTTCTTCTT 647
 QY 181 PheSerAlaValAlaPhePheTrpArgLysSerProIleGlyMetIleSerLeuAlaMetMet 200
 DB 648 TTCCTCGCGTTTCTTCTGAGAGAGATCTCTTACGTAAGATCTCGTTAGCAATATAG 707
 QY 201 CyseGlyLysPheGlyIleAlaSerPheMetGlyArgLysPheGlySerThriLysPro 220
 DB 708 TGTGTCGCGCATGAGAAATGCTGATATATGAGAGCTTAAGTTGGGTCACTTAATATCTT 767
 QY 221 TyrAnProlArgLysSerTrpAlaGlySerIleSerMetPheIlePheGlyPhePheIle 240
 DB 768 TACAAACCAAGAAAGATGGGAGAGATCTTCATGCTTCATCTTCGCTTCTCATC 827

QY 241 SerIleAlaLeuLeuTYTYrSerSerLeuGlyTyrLeuHisMetAenTrpGluThr 260
 DB 828 TCCATCGATTAATCTTATCTTATCTCAAGCCTTGGGACTTCAACAGAACTGGGAAACG 887
 QY 261 ThrLeuGlnArgValAlaMetValSerMetValAlaThrValAlaGlnSerLeuProIle 280
 DB 888 ACCTTGACAGAGAGAGAAAGGTCCTCAATGTCGCAAGGAGTCGATGCTTACCCATC 947
 QY 281 ThrArgGlnLeuAlaPhePheAnIleSerValProlLeuAlaThrIleLeuAlaAlaTyrLeu 300
 DB 948 ACCATCAATTAAGACGACAAATATTCGTTCTCTGCTGCTACTATTAATTAATTAATTA 1007
 QY 301 SerPheGlyTyr 304
 DB 1008 AGTTGCGATAT 1019
 RESULT 3
 ADX31786
 ID ADX31786 standard; cDNA; 980 BP.
 XX
 AC ADX31786;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Plant full length insert polynucleotide seqid 14606.
 XX
 KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomanan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.
 XX
 OS Unidentified.
 XX
 PN US2004034888-A1.
 XX
 PD 19-FEB-2004.
 XX
 PF 28-APR-2003; 2003US-00425114.
 XX
 PR 06-MAY-1999; 99US-00304517.
 XX
 PR 05-NOV-2001; 2001US-00985678.
 XX
 PA (LIU/J) LIU J.
 PA (ZHOU/J) ZHOU Y.
 PA (KOVA/J) KOVALIC D K.
 PA (SCREEN/J) SCREEN S E.
 PA (TABASKA/J) TABASKA J E.
 PA (CAO/Y) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX
 DR WPI; 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 14606; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid=2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in

CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactamannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.

XX SQ Sequence 980 BP; 223 A; 229 G; 215 G; 313 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,87e-164	Length:	980
Score:	1523.00	Matches:	301
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.2%	Indels:	0
DB:	13	Gaps:	0

US-10-634-548-2 (1-304) x ADX31786 (1-980)

QY 4 ThrLeuProLeuSerProIleAsnHisGlnLeuCysArgPheGlyAsnAsnSerLeuThr 23
 DB 3 ACCTTACCTTATCTCCGATCATCATCATGTTGTGCGGTTCCGGAACAACCTTTGACG 62
 QY 24 ThrHisArgPheCysSerProGlyPheLeuIleSerProCysPheIleGlyLeuThr 43
 DB 63 ACTCACCGGTCCTTCTCCGCGCTTCTTGATTTCTTCTTCTTCTTCTTCTTCTTCAAC 122
 QY 44 GlyMetGlySerAlaThrGlnLeuArgAlaArgArgSerLeuIleSerSerAlaValAla 63
 DB 123 GGAATGGGCTTCTGCTACCTTACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCG 182
 QY 64 ThrAsnSerLeuLeuHisAspValGlyAlaThrValAlaValLeuGlyValAlaTyrAla 83
 DB 183 ACGAATTCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 242
 QY 84 LeuValLeuSerPheGlySerLeuThrIleArgAsnValIleGlnGlnSerLeuSerArg 103
 DB 243 CTTGCTTAAAGCTTCAAGAGTCTCAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 302
 QY 104 LysLeuValHisIleLeuSerGlyLeuLeuPheValLeuAlaTyrProIlePheSerGly 123
 DB 303 AAGCTTGGCATATCTCAAGTCTGCTTTCGTAAGTCTGCTGCTGCTGCTGCTGCTGCTG 362
 QY 124 SerThrGlnAlaArgTyrPheAlaAlaPheValProLeuValLeuGlyLeuArgLeuVal 143
 DB 363 TCGACCGAGGCTCGATACCTTGTGCTGCTTGTTCGTTAGCAATGCGCTTAAAGCTTGT 422
 QY 144 IleAsnGlyLeuSerIleSerProAsnSerMetLeuIleLysSerValIleThrArgGlnGly 163
 DB 423 ATTTAACGAGATATCATTTCCCAATTCGATGCTAATCAATCCGTCACAAGAGAGAGG 482
 QY 164 ArgAlaGlnGlyLeuLeuValGlyPheLeuPheTyrValLeuAlaLeuLeuPheSerAla 183
 DB 483 AGACAGAGAGAGTCTTAAAGTCTTGTCTTCAAGTCTTCAAGTCTTCTTCTGCGG 542
 QY 184 ValPhePheTyrArgGlySerProIleGlyMetIleSerLeuAlaMetMetCysGlyGly 203
 DB 543 GTTTCTCTCGAGAGAGTCTCTATCGGTATGATCTCGTTAGCAATGATGATGATGATG 602
 QY 204 AspGlyIleAlaAspIleMetGlyArgArgPheGlySerThrIleValIleProTyrAsnPro 223
 DB 603 GATGGAATAGCTGATATATGAGAGAGATTTGGGTAACTTAAGATACCTTACCAACCA 662
 QY 224 ArgLysSerTyrAlaGlySerIleSerMetPheIlePheGlyPhePheIleSerIleAla 243
 DB 663 AGAAGAGATTTGGGAGAGAGATCTCAATGTTCACTTCGCTTCTTCAATCTCCATCCCA 722
 QY 244 LeuLeuTyrTyrTyrSerSerLeuGlyTyrLeuHisMetAsnTyrGluThrLeuGln 263

DB 723 TTACTTACTATTATTCACAGCCTTGGGTACTTACATGAATCTGGGAACGACCTTGACG 782
 QY 264 ArgValAlaMetValSerMetValAlaThrValValGlySerLeuProIleThrAspGln 283
 DB 783 AGGTGCAATGATCTTCATGTGTCGCGACGATGTCGATGATGATGATGATGATGATGATG 842
 QY 284 LeuAspAspAsnIleSerValProLeuAlaThrIleLeuAlaAlaTyrLeuSerPheGly 303
 DB 843 TTAGACGACAAATTTTCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 902
 QY 304 Tyr 304
 DB 903 TAT 905
 RESULT 4
 AAC36634
 ID AAC36634 standard; DNA; 1088 BP.
 XX AAC36634;
 AC 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana DNA fragment SBQ ID NO: 14519.
 XX
 KM Hybridisation assay; genetic mapping; gene expression control;
 KM protein identification; signal transduction pathway; metabolic pathway;
 KM promoter; termination sequence; ss.
 XX Arabidopsis thaliana.
 XX EP1033405-A2.
 PN 06-SEP-2000.
 PD
 XX 25-FEB-2000; 2000EP-00301439.
 PF
 XX 25-FEB-1999; 99US-0121825P.
 XX 05-MAR-1999; 99US-0123180P.
 XX 09-MAR-1999; 99US-0123548P.
 XX 23-MAR-1999; 99US-0125788P.
 XX 25-MAR-1999; 99US-0126264P.
 XX 29-MAR-1999; 99US-0126785P.
 XX 01-APR-1999; 99US-0127462P.
 XX 06-APR-1999; 99US-0128234P.
 XX 08-APR-1999; 99US-0128714P.
 XX 16-APR-1999; 99US-0129845P.
 XX 19-APR-1999; 99US-0130077P.
 XX 21-APR-1999; 99US-0130449P.
 XX 23-APR-1999; 99US-0130510P.
 XX 28-APR-1999; 99US-0130891P.
 XX 30-APR-1999; 99US-0131449P.
 XX 30-APR-1999; 99US-0132048P.
 XX 30-APR-1999; 99US-0132407P.
 XX 04-MAY-1999; 99US-0132484P.
 XX 05-MAY-1999; 99US-0132485P.
 XX 06-MAY-1999; 99US-0132486P.
 XX 07-MAY-1999; 99US-0132487P.
 XX 11-MAY-1999; 99US-0134256P.
 XX 14-MAY-1999; 99US-0134218P.
 XX 14-MAY-1999; 99US-0134219P.
 XX 14-MAY-1999; 99US-0134221P.
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 XX 18-MAY-1999; 99US-0134768P.
 XX 19-MAY-1999; 99US-0134941P.
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 XX 21-MAY-1999; 99US-0135329P.
 XX 24-MAY-1999; 99US-0135629P.
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 XX 27-MAY-1999; 99US-0136392P.
 XX 28-MAY-1999; 99US-0136782P.
 XX 01-JUN-1999; 99US-0137222P.
 XX 03-JUN-1999; 99US-0137528P.

PR 04-JUN-1999;	99US-0137502P.	PR 06-AUG-1999;	99US-0147303P.
PR 07-JUN-1999;	99US-0137724P.	PR 06-AUG-1999;	99US-0147416P.
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PR 10-JUN-1999;	99US-0138847P.	PR 10-AUG-1999;	99US-0148171P.
PR 14-JUN-1999;	99US-0139119P.	PR 11-AUG-1999;	99US-0148319P.
PR 16-JUN-1999;	99US-0139452P.	PR 12-AUG-1999;	99US-0148341P.
PR 16-JUN-1999;	99US-0139453P.	PR 13-AUG-1999;	99US-0148565P.
PR 17-JUN-1999;	99US-0139492P.	PR 13-AUG-1999;	99US-0148684P.
PR 18-JUN-1999;	99US-0139454P.	PR 16-AUG-1999;	99US-0149368P.
PR 18-JUN-1999;	99US-0139455P.	PR 17-AUG-1999;	99US-0149175P.
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PR 18-JUN-1999;	99US-0139461P.	PR 23-AUG-1999;	99US-0149930P.
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PR 18-JUN-1999;	99US-0139763P.	PR 27-AUG-1999;	99US-0151066P.
PR 21-JUN-1999;	99US-0139817P.	PR 27-AUG-1999;	99US-0151080P.
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PR 23-JUN-1999;	99US-0140353P.	PR 31-AUG-1999;	99US-0151438P.
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PR 02-JUL-1999;	99US-0142055P.	PR 22-SEP-1999;	99US-0155139P.
PR 06-JUL-1999;	99US-0142390P.	PR 23-SEP-1999;	99US-0155486P.
PR 08-JUL-1999;	99US-0142803P.	PR 24-SEP-1999;	99US-0155659P.
PR 09-JUL-1999;	99US-0142920P.	PR 28-SEP-1999;	99US-0156458P.
PR 12-JUL-1999;	99US-0142977P.	PR 29-SEP-1999;	99US-0156596P.
PR 13-JUL-1999;	99US-0143542P.	PR 04-OCT-1999;	99US-0157117P.
PR 14-JUL-1999;	99US-0143623P.	PR 05-OCT-1999;	99US-0157753P.
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PR 19-JUL-1999;	99US-0144325P.	PR 12-OCT-1999;	99US-0158369P.
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PR 19-JUL-1999;	99US-0144333P.	PR 13-OCT-1999;	99US-0159285P.
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PR 19-JUL-1999;	99US-0144335P.	PR 14-OCT-1999;	99US-0159637P.
PR 20-JUL-1999;	99US-0144632P.	PR 14-OCT-1999;	99US-0159637P.
PR 20-JUL-1999;	99US-0144884P.	PR 14-OCT-1999;	99US-0159638P.
PR 21-JUL-1999;	99US-0144881P.	PR 18-OCT-1999;	99US-0159584P.
PR 21-JUL-1999;	99US-0145086P.	PR 21-OCT-1999;	99US-0160741P.
PR 21-JUL-1999;	99US-0145088P.	PR 21-OCT-1999;	99US-0160767P.
PR 22-JUL-1999;	99US-0145085P.	PR 21-OCT-1999;	99US-0160768P.
PR 22-JUL-1999;	99US-0145087P.	PR 21-OCT-1999;	99US-0160770P.
PR 22-JUL-1999;	99US-0145089P.	PR 21-OCT-1999;	99US-0160770P.
PR 22-JUL-1999;	99US-0145192P.	PR 21-OCT-1999;	99US-0160815P.
PR 23-JUL-1999;	99US-0145145P.	PR 22-OCT-1999;	99US-0160980P.
PR 23-JUL-1999;	99US-0145218P.	PR 22-OCT-1999;	99US-0160981P.
PR 23-JUL-1999;	99US-0145224P.	PR 22-OCT-1999;	99US-0160989P.
PR 26-JUL-1999;	99US-0145276P.	PR 25-OCT-1999;	99US-0161404P.
PR 27-JUL-1999;	99US-0145913P.	PR 25-OCT-1999;	99US-0161405P.
PR 27-JUL-1999;	99US-0145918P.	PR 25-OCT-1999;	99US-0161406P.
PR 27-JUL-1999;	99US-0145919P.	PR 26-OCT-1999;	99US-0161359P.
PR 28-JUL-1999;	99US-0145951P.	PR 26-OCT-1999;	99US-0161360P.
PR 02-AUG-1999;	99US-0146386P.	PR 26-OCT-1999;	99US-0161361P.
PR 02-AUG-1999;	99US-0146388P.	PR 28-OCT-1999;	99US-0161920P.
PR 03-AUG-1999;	99US-0147038P.	PR 28-OCT-1999;	99US-0161922P.
PR 04-AUG-1999;	99US-0147204P.	PR 28-OCT-1999;	99US-0161993P.
PR 05-AUG-1999;	99US-0147192P.	PR 29-OCT-1999;	99US-0162142P.
PR 05-AUG-1999;	99US-0147260P.		

Alignment Scores:
Pred. No.:

3.36e-164

Length:

1088

Score: 1523.00 Matches: 300
 Percent Similarity: 99.7% Conservative: 3
 Best Local Similarity: 98.7% Mismatches: 1
 Query Match: 99.2% Indels: 0
 DB: 3 Gaps: 0

US-10-634-548-2 (1-304) x AAC36634 (1-1088)

QY 1 MetAlaAlaThrLeuProLeuSerProIleAsnHsGlnLeuCyArgPheGlyAsnAsn 20
 Db 108 ATGGCAGACACCTTAATCTATCCGATCAATCATAGTGTGTGGTGGGAAAC 167
 QY 21 SerLeuThrThiAsrPheCysSerProGlyPheLeuIleSerSerProCysPheIle 40
 Db 168 TCTTGAAGCATCAACGGCTCTGTCTCTGGCTTCTGATTCTTCTCTCTGTTTCAAT 227
 QY 41 GlyLeuThrGlyMetGlySerAlaThrGlnLeuArgAlaArgGlySerLeuIleSerSer 60
 Db 228 GGTTCACCGGAATGGGCTGTGCTACTCAAGTTACGTGCTGCTCTGATCTCTTCA 287
 QY 61 AlaValAlaThrAsnSerLeuLeuHsAspValGlyAlaThrValAlaValLeuGlyGly 80
 Db 288 GCAGTTGGAGCAATTCGCTGTGATGACGTCCGAGCCACGTCGTCGTCGTCGTCGTCG 347
 QY 81 AlaTyralaLeuValLeuSerPheGlySerLeuThrIlyAsrAsnValIleGlnGlnSer 100
 Db 348 GCATACCGCGCTTGTCTTAAGCTTCGAGAGTCTCACCAAGCAACGTCATTCACAGAGT 407
 QY 101 LeuSerArgIlybLeuValHsIleLeuSerGlyLeuLeuPheValLeuAlaTrpProIle 120
 Db 408 TTGAGCAGAAAGCTTGTGCATATACTCCAGGTCTGCTTTCGATCTTGCCTGCGCATC 467
 QY 121 PheSerGlySerThrGlyAlaArgTyrrPheAlaAlaPheValProLeuValAsnGlyLeu 140
 Db 468 TTCACCGATGCACCGAGCTCGATCTTGTGCTTGTTCCTTGTGTAAGGCTTA 527
 QY 141 ArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMetLeuIleLeuSerValThr 160
 Db 528 AGGCTGTGTTATTAACGACATATCCATTTCCCAATTCGATGCTAATCAATCCGTCACA 587
 QY 161 ArgGlyIlyArgAlaGlnGlnLeuLeuLeuGlyProLeuPheTyrrValLeuAlaLeuLeu 180
 Db 588 AGAGAAGGAGAGCAGAGAGTGTGTTAAAGTCTTGTGTTCTACGTTCTGAGCTTCTT 647
 QY 181 PheSerAlaValPhePheTrpArgGlySerProIleGlyMetIleSerLeuAlaMetMet 200
 Db 648 TTCTCTGCGGTTTCTTCTGAGAGAGTCTCTATCGATAGATCTCGTTAGCAATGATG 707
 QY 201 CysGlyIlyAspGlyIleAlaAspIleMetGlyArgIlyPheGlySerThrIlyIlePro 220
 Db 708 TGTGCTGGCGATGGATAGTGTGATTAATGGGACGTAAAGTTGGGTCAACTAAGATACCT 767
 QY 221 TyrAsnProArgIlybSerTrpAlaGlySerIleSerMetPheIlePheGlyPhePheIle 240
 Db 768 TACAACCCCAAAAGATTGGGCGAGAGCAATCTCAAGTTCATCTTGGCTTCTTCAATC 827
 QY 241 SerIleAlaLeuLeuTyrrTyrrSerSerLeuGlyTyrrLeuHsMetAsnTrpGlnThr 260
 Db 828 TCCATCGCATTAATCTTAATCACTACCAAGCCTTGAGTACCTTCACATTAACGGGAAACG 887
 QY 261 ThrLeuGlnArgValAlaMetValSerMetValAlaThrValAlaGlnSerLeuProIle 280
 Db 888 ACCTTGACGAGAGTATGATAGTCTCAATGTGACCAAGTGTGAGTGTGCTACCAATC 947
 QY 281 ThrAspGlnLeuAspAsnAlaSerValProLeuAlaThrIleLeuAlaAlaTyrrLeu 300
 Db 948 ACCGATCAATTAAGACAGACAGTTCGGTCTCTGCGACTAATTAATTAACGCTTATTTA 1007
 QY 301 SerPheGlyTyrr 304
 Db 1008 AGTTTCGATAT 1019

RESULT 5

ADJ98165
 ID ADJ98165 standard; DNA; 1897 BP.
 AC ADJ98165;
 XX 06-MAY-2004 (first entry)
 DT
 XX
 XX Thale cress LTT1 phytol kinase mutant DNA.
 XX
 XX phytol kinase; tocopherol biosynthesis; plant; drought resistance; LTT1;
 KM thale cress; ds; gene; mutant.
 XX
 XX Arabidopsis thaliana.
 PN MO2004013312-A2.
 XX
 PD 12-FEB-2004.
 XX
 XX 05-AUG-2003; 2003MO-US025276.
 PF
 XX 05-AUG-2002; 2002US-0400689P.
 PR 05-AUG-2003; 2003US-00634548.
 XX
 XX (MONS) MONSANTO TECHNOLOGY LLC.
 PA
 PI Norris SR, Lincoln K, Abad MS, Eilers R, Hartsuyker KK;
 PI Hirschberg J, Karunanandaa B, Moshiri F, Stein JC, Valentin HE;
 PI Venkatesh TV,
 PI
 XX WPI; 2004-157125/15.
 DR
 XX P-PSDB; ADJ98166.
 XX
 XX New phytol kinase polynucleotides, useful in mediating tocopherol
 PT biosynthesis and in producing plants with increased drought resistance.
 PT
 XX
 XX Example 2; SEQ ID NO 3; 189pp; English.
 PS
 XX The invention relates to a novel substantially purified nucleic acid
 CC molecule encoding a phytol kinase. The nucleic acid molecules and
 CC polypeptides of the invention may be useful in mediating tocopherol
 CC biosynthesis and in producing plants with increased drought resistance.
 CC The current sequence is that of the thale cress LTT1 phytol kinase mutant
 CC DNA of the invention.
 CC
 XX
 SQ Sequence 1897 BP; 501 A; 408 C; 332 G; 656 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.7e-136 Length: 1897
 Score: 1284.50 Matches: 301
 Percent Similarity: 52.4% Conservative: 0
 Best Local Similarity: 52.4% Mismatches: 3
 Query Match: 83.6% Indels: 272
 DB: 12 Gaps: 5
 US-10-634-548-2 (1-304) x ADJ98165 (1-1897)
 QY 1 MetAlaAlaThrLeuProLeuSerProIleAsnHsGlnLeuCyArgPheGlyAsnAsn 20
 Db 108 ATGGCAGACACCTTAATCTATCCGATCAATCATAGTGTGTGGTGGGAAAC 167
 QY 21 SerLeuThrThiAsrPheCysSerProGlyPheLeuIleSerSerProCysPheIle 40
 Db 168 TCTTGAAGCATCAACGGCTCTGTCTCTGGCTTCTGATTCTTCTCTGTTTCAAT 227
 QY 41 GlyLeuThrGlyMetGlySerAlaThrGlnLeuArgAlaArgGlySerLeuIleSerSer 60
 Db 228 GGTTCACCGGAATGGGCTGTGCTACTCAAGTTACGTGCTGCTCTGATCTCTTCA 287
 QY 61 AlaValAlaThrAsnSerLeuLeuHsAspValGlyAlaThrValAlaValLeuGlyGly 80
 Db 288 GCAGTTGGAGCAATTCGCTGTGATGACGTCCGAGCCACGTCGTCGTCGTCGTCGTCG 347
 QY 81 AlaTyralaLeuValLeuSerPheGlySerLeuThrIlyAsrAsnValIleGln----- 98

```

Db      348 GCATCGCGCTTGTCTTAAGCTTCAGAGTCTCAACCAAGCAAGCTATTCACAGGTC 407
Qy      98 -----
Db      408 TCTTAATATGCTTTAGTATCCACAAATTTCTCGTTTACATTCAGTTTATTCG 467
Qy      98 -----
Db      468 AACCACTATATGTTGAAGAAGTTCTCAAGTTGTGTTCAGTACTACTATAGAA 527
Qy      98 -----
Db      528 ACAATGATAGCCTAGAAATTTGTGTGAATTAAGTTTTCATTCGAATTTTATAA 587
Qy      98 -----
Db      588 GAATTTGTACACCTTAGTAAGAGTATACCACTTTATCATGACCAATCGGTAAAGCGGA 647
Qy      98 -----
Db      648 CAAGAACAAAGTGTCCAAAAATTTATACCGCTTATATGTTACCACTTTCTTAACCTC 707
Qy      98 -----
Db      708 CTTTAACTATCCGTATCCGCTACCGCTAAACATATACCGTCTTGTGTAAACA 767
Qy      99 -----
Db      768 AAGTAAAGAAAGAAACAAATACCTTGAATGTTTATGATGAGCAGAGTTGAGCAG 827
Qy      103 glyleuValHisIleLeuSerGlyLeuLeuPheValIleuAlaTyrProIle----- 120
Db      828 AAAGCTTGATGATACTCTGACGCTGCTTGTCTGACTCTGCGGCCAAATCTTCAGGTA 887
Qy      120 -----
Db      888 TTGCTTCTCTATGTTTGTAAATCTCTGTAACCTTTAAACATATAGCATTCGA 947
Qy      121 -----
Db      948 TTTCTTTTACTCATCTTAAAGTTCGCGATCCGACGAGCTCGATCTTGTGCGCTTT 1007
Qy      133 eValProIleuValIleuArgLeuValIleuArgIleuSerIleSerProIleSe 153
Db      1008 TGTTCGTTAGTGAATGCTTAAGGCTTGTATTAACGACATTCATTTCCCAAAATTC 1067
Qy      153 rMetLeuIleIleuSerValThrArgGluGlyArgAlaGlu----- 166
Db      1068 GATGCTAATCAAAATCCGTCACAGAGAGAGAGAGAGTATGTTGTTT 1127
Qy      166 -----
Db      1128 TCCAACCTTGATGATATTTTCAACAATCTGATTAACATTTCTGTTTCCAAACATCA 1187
Qy      167 -----
Db      1188 CAGAGAGTGTCTTAAGGCTCTTGTGTCTTACGTTCTTCTTCTCTGCGGTTTT 1247
Qy      185 ePheTrpArgGluSerProIleGlyMetIleSerLeuAlaMetCysGlyGlyAspGI 205
Db      1248 CTTCTGAGAGAGTCTCTATCGATATCTCTGTTAGCATGATGTGTGTGCGAGATG 1307
Qy      205 yIle----- 206
Db      1308 TAA-ATTTCTGCAAGTACTACTGTATATTAATTAATTAACAATTAAGCGCATAA 1366
Qy      207 -----
Db      1367 ATGTACTAATAAGTCTGCATCAATATGCTATAGTAAGAAATAGCTGATTAATAGGACG 1426
Qy      212 glyPheGlySerThrIleuValIleProIleAspProArgIleSerTrpAlaGlySerIleSe 232

```

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Db      1427 TAAGTTGGTCAACTAAGATACCTTAACACCAAGAAAGATTAGCAGAGACATCTC 1486
Qy      232 rMetPheIlePheGlyPhePheIleSerIleAla----- 243
Db      1487 CATGTTATCTTCGGCTTCTTCATCTCCATTCGC-GTAAAAATATTAACCAATCCATATT 1545
Qy      243 ----- 243
Db      1546 AATCATAAATATGCTCTCTTTCAGACAGCAAGATCTTAAGAACTGATGATTCG 1605
Qy      244 -----
Db      1606 TACTAAACCTTAACGCTTTTCTTTGTAATTTTGACAGATTAATTAATTAATTAATTA 1665
Qy      251 uGlyIleuHisMetLeuTrpGluThrThrLeuGlnArgValAlaMetValSerMetVa 271
Db      1666 TGGGTACTCTCACTGAACTGGAAGAACCTTTCAGAGATACCAATGCTCAATGCT 1725
Qy      271 AlaThrValValGluSerLeuProIleThrAspGlnLeuAspAspAsnIleSerValPr 291
Db      1726 CGCAACGCTAGTCCAGTCCGCTAACCCATCACCGATCAATTAAGACGACATATTTGGTTCC 1785
Qy      291 OLeuAlaThrIleLeuAlaAlaIleuSerPheGlyTyr 304
Db      1786 TCTGCTACTATTTTACGCTTATTAAGTTTCGATAT 1825

RESULT 6
ADXS4389
ID ADXS4389 standard; cDNA; 1062 BP.
AC ADXS4389;
DC 21-APR-2005 (first entry)
DE
DM
DN
DT
DX
EY
FZ
GZ
HZ
IY
JZ
KZ
LZ
MZ
NZ
OZ
PZ
QZ
RZ
SZ
TZ
UZ
VZ
WZ
XZ
YZ
ZZ
US2004034888-A1.
PD 19-FEB-2004.
PP 28-APR-2003; 2003US-00425114.
PR 06-MAY-1999; 99US-00304517.
PS 05-NOV-2001; 2001US-00985678.

(LIU/J.) LIU J.
(PA) (ZHOU Y.) ZHOU Y.
(PA) (KOVAN/J.) KOVALIC D K.
(PA) (SCREB/J.) SCREEN S E.
(PA) (TABASKA/J.) TABASKA J E.
(PA) (CAO Y.) CAO Y.

Liu J, Zhou Y, Kovajic DK, Screen SE, Tabaska JE, Cao Y;
WPI; 2004-180133/17.

New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
XX improving yield.
PS Claim 1; SEQ ID NO 29129; 15pp; English.

```

XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp://data.uspto.gov/sequence.html?docID=2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.

Sequence 1062 BP; 235 A; 264 C; 243 G; 320 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
9.39e-135	1266.00	1062	250
Percent Similarity:	89.3%	Conservative:	24
Best Local Similarity:	81.4%	Mismatches:	27
Query Match:	82.4%	Indels:	6
DB:	13	Gaps:	2

US-10-634-548-2 (1-304) x ADX54389 (1-1062)

QY 1 MetAlaAlaThrLeuProLeuSerProIleAsnHisGlnLeuCyAArgPheGlyAAsnAsn 20
 DB 46 ATGGCGGACGCTTATCTTATCTCCGCTTACCCATCGATCGATTATGCGATAGACACAGG 105
 QY 21 -----SerLeuThrThrHisArgPheCySerProGlyPheLeuIleSerSerPro 37
 DB 106 TTCTGTATTAACGATATGATCCCGGTTCTGTTGCGCA-----GTTTCTTCGCGCC 156
 QY 38 CysPheIleGlyLeuThrGlyMetGlySerAlaThrGlnLeuAArgAlaArgSerLeu 57
 DB 157 TGTTCATCGCGCGTAAAGAAATCGGCTGTCGACATCGATTACGGGCTCGCACCTCTG 216
 QY 58 ILeSerSerAlaValAlaThrAsnSerLeuHisAspValGlyAlaThrValAlaVal 77
 DB 217 ATCTCTTACGCGGCTTCATCATATTAATGATGACGTGACGACGACGATGCGCACTT 276
 QY 78 LeuGlyGlyAlaTyrAlaLeuValLeuSerPheGlnSerLeuThrLysArgAsnValIle 97
 DB 277 CTTAGTGGTGCCTTACGCGCTTGTCTTACTCTTCAGAGTCTCAAGACGAGACGTCGATT 336
 QY 98 GlnGlnSerLeuSerArgLysLeuValHisIleLeuSerGlyLeuLeuPheValLeuAla 117
 DB 337 CCACGAGATTGAGAGAAAGCTTGTGATATATCTCAGGCTGCTTTGCGGCTCTCG 396
 QY 118 TrpProIlePheSerGlySerThrGlnAlaArgTyrPheAlaAlaPheValProLeuVal 137
 DB 397 TGGCCAACTTCACGCGCATCAACGAGGCTGATCTTTCGCTGTTTCTTCCTTATG 456
 QY 138 AsnGlyLeuArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMetLeuIleLys 157
 DB 457 AATGGCTTAAGGCTTGTGTCAACGTTTGTCTCCCTCCCTAATCCACGCTAATCCAA 516
 QY 158 SerValThrArgGlnGlyArgAlaGlnGlnLeuLysGlyProLeuPheValValLeu 177
 DB 517 TCCGTAAGTACGAGGAGAAACCAAGAGATTGCTTAAAGTCCATTGCTTACCTTCA 576
 QY 178 AlaLeuLeuPheSerAlaValPhePheTrpArgGlnSerProIleGlyMetIleSerLeu 197
 DB 577 GCCCTTCTAGTGTCTGCAAGTTTCTTCTGAGAGATTCTCCACCGGATATATACGCTG 636
 QY 198 AlaMetMetCysGlyGlyAspGlyIleAlaAspIleMetGlyArgLysPheGlySerThr 217

DB 637 GCATATGTGTGTGGTGGCGACGAAATAGCTGATATCAATGGACGTATGATCATATAC 696
 QY 218 LysIleProTyrAsnProArgLysSerTrpAlaGlySerIleSerMetPheIlePheGly 237
 DB 697 AAGTATCTTACCAACCAACCAAGAAAGCTTGGCGGAGACATCTTCATCTTATTTGGC 756
 QY 238 PhePheIleSerIleAlaLeuLeuTyrTyrTyrSerSerLeuGlyTyrLeuHisMetAsn 257
 DB 757 TTCTTATCTTCATCCATCGGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 816
 QY 258 TrpGlnThrThrLeuGlnArgValAlaMetValSerMetValAlaThrValAlaGlnSer 277
 DB 817 TGGGAAACCAACCTTTACGAGAGTCCGATTTGTCTCATTTGTCGCTACGTTGGTGA 876
 QY 278 LeuProIleThrAspGlnLeuAspAspAsnIleSerValProLeuAlaThrIleLeuAla 297
 DB 877 CTACCCATCAACCGATCAAAATAGACGACAGATTCGATTCTCTGCGTACTATTTGGCT 936
 QY 298 AlaTyrLeuSerPheGlyTyr 304
 DB 937 GCTTACCTAAGTTTGGATAT 957

RESULT 7

ADX45670
 ID ADX45670 standard; cDNA; 1007 BP.
 AC ADX45670;
 XX 21-APR-2005 (first entry)
 DT
 XX
 XX Plant full length insert polynucleotide seqid 20410.
 DE
 XX plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.
 XX
 OS unidentified.
 XX
 XX US200403488-A1.
 XX
 XX 19-FEB-2004.
 XX
 XX 28-APR-2003; 2003US-00425114.
 XX
 XX 06-MAY-1999; 99US-00304517.
 XX
 XX 05-NOV-2001; 2001US-00985678.
 XX
 XX (LNU/) LNU J.
 XX (ZHOV/) ZHOV Y.
 XX (KOVA/) KOVALIC D K.
 XX (SCRE/) SCREEN S E.
 XX (TABA/) TABASKA J E.
 XX (CAOV/) CAO Y.
 XX
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 XX
 XX New recombinant DNA construct, useful for improving plant tolerance to
 XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 XX pests, for conferring increased resistance to plant disease, or for
 XX improving yield.
 XX
 XX Claim 1; SEQ ID NO 20410; 15pp; English.
 XX
 XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence

CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.

XX
 SQ Sequence 798 BP; 159 A; 195 C; 223 G; 221 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9,13e-79	Length:	798
Score:	776.00	Matches:	143
Percent Similarity:	80.2%	Conservative:	52
Best Local Similarity:	58.8%	Mismatches:	48
Query Match:	50.5%	Indels:	0
DB:	13	Gaps:	0

US-10-634-548-2 (1-304) x ADX48515 (1-798)

```

QY 60 SerAlaValAlaThrAsnSerLeuLeuHisAspValGlyAlaThrValAlaValLeuGly 79
   |||||
DB 1 GCGGCCGCGCGCCGCCGCGGCTGACGAGCGGAGCGGCTACGTGCTCATCCGCC 60
   |||||
QY 80 GlyAlaTyrAlaLeuValLeuSerPheGlnSerLeuThrTyrArgAsnValIleGlnGln 99
   |||||
DB 61 GCGCGCTTCTCTTGTGTGCGCGCTTTCACGAGCTCACGAGCGGCGGCTCATCCAGAAAG 120
   |||||
QY 100 SerLeuSerArgLeuValHisIleLeuSerGlyLeuLeuPheValLeuAlaTyrPro 119
   |||||
DB 121 AGCTTGAGCAGAGAGAGGTTGTGACGCTATCCGGGCTGCTGTTATGTCATCATCTGGCCC 180
   |||||
QY 120 IlePheSerGlySerThrGlnIleArgTyrPheAlaAlaPheValProLeuValIleGly 139
   |||||
DB 181 CTGTTGAGAAATTCGACGAGAGCGATTTGCGCGGCTTGTCCCTGCTTGAATCTC 240
   |||||
QY 140 LeuArgLeuValIleHisGlyLeuSerIleSerProHisSerMetLeuIleLysSerVal 159
   |||||
DB 241 ATGAGGCTTCTGATATATGAGATCCGCTCTACACGATGAGAGCTCTGTAAATCAGTG 300
   |||||
QY 160 ThrArgGlyGlyArgAlaGlnGlnLeuLeuGlyGlyProLeuPheTyrValLeuAlaLeu 179
   |||||
DB 301 ACACGCGAAGAAACACAGAGGATTCGAGAGGCTCCATCTATATGCTGTGCTG 360
   |||||
QY 180 LeuPheSerAlaValPhePheTyrPargIleSerProIleGlyMetIleSerLeuAlaMet 199
   |||||
DB 361 CTGTTGAGGCTTCTGATATATGAGATCCGCTCTACACGATGAGAGCTCTGTAAATCAGTG 420
   |||||
QY 200 MetCysGlyGlyAspGlyIleAlaAspIleMetGlyArgLysPheGlySerThrIysIle 219
   |||||
DB 421 ATGAGCGGAGCGGATGTTGCTGACATTTGTTGGAGGATATGCTCAGCGAAAGCTG 480
   |||||
QY 220 ProTyrAsnProArgLysSerTyrAlaGlySerIleSerMetPheIlePheGlyPhePhe 239
   |||||
DB 481 CCAATTCATCCGAAAGAGAGCTGGGCGGAGAGCATCTCATATGTTCTGCTTCCGTTCC 540
   |||||
QY 240 IleSerIleAlaLeuLeuTyrTyrTyrSerSerSerLeuGlyTyrLeuHisMetAsnTyrGln 259
   |||||
DB 541 CTGTCGCCAGTATGAGTCTTCTACTTCAAGCTCGGATTCATTTATGTTATCTATCTGAGAA 600
   |||||
QY 260 ThrThrLeuGlnArgValAlaMetValSerMetValAlaThrValValAlaGlnSerLeuPro 279
   |||||
DB 601 GAGGCACTTGTAAGTGGGCTGTTGTCATGACGAGCGAGCATGATGAGAGCGCTTCT 660
   |||||
QY 280 IleThrAspGlnLeuAspAspAsnIleSerValProLeuAlaThrIleLeuAlaIleTyr 299
   |||||
DB 661 GTGACCGAAGTGTAGATGCAACATATATGTTCTTGTGGCCACATGCTGTAGTCTT 720
   |||||
QY 300 LeuSerPhe 302
   |||||
DB 721 CTCTTGT 729

```

RESULT 11

```

ADX51811
ID ADX51811 standard; cDNA; 976 BP.
XX
AC ADX51811;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 26551.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
XX
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ)/ LIU J.
PA (ZHOU)/ ZHOU Y.
PA (KOVA)/ KOVALIC D K.
PA (SCRE)/ SCREEN S E.
PA (TABAS)/ TABASKA J E.
PA (CAOY)/ CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 26551; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 976 BP; 149 A; 300 C; 280 G; 247 T; 0 U; 0 Other;
XX

```

Alignment Scores:

Pred. No.:	2,72e-78	Length:	976
Score:	773.00	Matches:	149
Percent Similarity:	70.9%	Conservative:	56
Best Local Similarity:	51.6%	Mismatches:	66

```

Query Match:      50.3%      Indels:      18
DB:               13        Gaps:         1
US-10-634-548-2 (1-304) x ADX51811 (1-976)

QY      33 LeuIIeSerSerProCyPheHeIIeGlyLeuThrGIyMeCGLySerAlaThrGIleuArg 52
DB      60 CTCCTCCTCCTCCCGACCTGCGTGCCTCGGGCGCTCCACCTCCGCCCCGACCTCGGC 119
QY      53 AlaArgArg----- 55
DB      120 GCCCGAGGCGCGAGCGGTGCTGCTCGCGCGCGCGCTCCGCGCTGCGCGGCGCG 179
QY      56 ---SerLeuIIeSerSerAlaValAlaThrAnsSerLeuHeIIaPheValAlaThr 74
DB      180 CTGGGCGGCTCGGCTTCGACGCGCGCGCGCTCCATGCTCTCGGAGCGGCGCGCGCACG 239
QY      75 ValAlaValaLeuGlyGIyAlaTyrAlaLeuValaLeuSerPheGluSerLeuThrIyArg 94
DB      240 CTGCTCGTACCGCGCGGCGCATCTCCCTCGCGCGCGCTTCGACGCGCTCCACGACGCG 299
QY      95 AnuValIIeGlnGlnSerLeuSerArgIyLeuValaHeIIeLeuSerGIyLeuLeuPhe 114
DB      300 CGCCTCGTCCACAGAGCTTGAGCAGAGAGTGTGCTGCTATCCGCGGCTCTTTTTC 359
QY      115 ValaLeuAlaTyrProIIePheSerGIySerThrGIuAlaArgTyrPheAlaIaPheVal 134
DB      360 ATGGCTTCATGGCCACTTCTTCAGCAATCTTACAGTGCAGGCTGCTGCGAGCGGTAGT 419
QY      135 ProLeuValaAnGlyLeuArgLeuValaIIeAnGlyLeuSerIleSerProAnSerMet 154
DB      420 CCGTTCCTGACATGGGTAGGCTTCTCACTACGCGGCTCGGCTTCTACTCCGACGAGCT 479
QY      155 LeuIIeLySerValaThrArgGluGIyArgAlaGluGluLeuLeuLyGIyProLeuPhe 174
DB      480 CTAGTAAATCGGTGACCCGCTGACAGAAACAGAGAGTATGCTCGAGGCGCTCTGTAC 539
QY      175 TyrValaLeuAlaLeuLeuPheSerAlaValaPhePheTTPArgGluSerProIIeLyMet 194
DB      540 TATGTCATCGTCTCTATGATCTGTTCTTATGCTTTTGGCGGAGCTCCCGCATCGAGTTC 599
QY      195 IleSerLeuAlaMetMetCyseGIyGIyAnArgIyIIeAlaPheIIeMetGIyArgIyPhe 214
DB      600 GTTTCCTTGTCATATAGACGCTGTGACGCGCTTTCGACATTTCTCGGAGAGAGTTC 659
QY      215 GlySerThrIyPheIleProTyrAnbProArgIySerTTPAlaGlySerIleSerMetPhe 234
DB      660 GCGTGGCTCAAGCTCCATTCAACAAGAGAGAGTGGGTGGGAGTGCAGATGTTTC 719
QY      235 IlePheGlyPhePheIleSerIleAlaLeuLeuTyrTyrTyrSerSerLeuGlyTyrLeu 254
DB      720 ATCTGTGGTTCCTCTCTATGCTGACTGATGCTGCTCTTCTCTGCTGGCTTGTATCATC 779
QY      255 HisMetAnuTTPGIuThrThrLeuGlnArgValaIaMetValaSerMetValaIaThrVal 274
DB      780 CATGTCACCTGGAGATCAGCGCGCTTGTGTAACGTGTTCTGCGCTGCGACCGACTGTG 839
QY      275 ValGluSerLeuProIIeThrAnPheIleuAnPheAnuIIeSerValProLeuAlaThr 294
DB      840 GTGGAGTGTATTCGTGAATCATGTGTGATGATGACATATCTGTTCCCTTGGCCACC 899
QY      295 IleLeuAlaAlaTyrLeuSerPheGly 303
DB      900 ATGTGTGTAAGCTTCTGTGTGTTCG 926

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DE      Plant full length insert polynucleotide seqid 25671.
XX      KM plant protectant; plant growth regulant; gene therapy; plant;
XX      KM recombinant DNA construct; physical array; plant breeding marker;
XX      KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX      KM extreme osmotic condition; pathogen tolerance; pest tolerance;
XX      KM growth rate; cell cycle pathway; disease resistance;
XX      KM galactomannan production; lignin production; plant growth regulator;
XX      KM yield; plant growth; plant development; seed oil; protein yield;
XX      KM protein content; gene; ss.
XX      OS Undifferentiated.
XX      PN US2004034888-A1.
XX      PD 19-FEB-2004.
XX      PF 28-APR-2003; 2003US-00425114.
XX      PR 06-MAY-1999; 99US-00304517.
XX      PR 05-NOV-2001; 2001US-00985678.
XX      PA (LITUJ/) LIU J.
XX      PA (ZHOU/) ZHOU Y.
XX      PA (KOVA/) KOVALIC D K.
XX      PA (SCRE/) SCREEN S E.
XX      PA (TABAK/) TABASKA J E.
XX      PA (CAO/) CAO Y.
XX      PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX      DR WPI, 2004-180133/17.
XX      PT New recombinant DNA construct, useful for improving plant tolerance to
XX      PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX      PT pests, for conferring increased resistance to plant disease, or for
XX      PT improving yield.
XX      PS Claim 1; SEQ ID NO 25671; 15bp; English.
XX      CC The invention describes a recombinant DNA construct comprising a
XX      CC polynucleotide consisting of a sequence encoding an amino acid sequence
XX      CC available in electronic form from the US patent office at
XX      CC ftp://seeddata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
XX      CC of the invention are also useful in physical arrays of molecules and as
XX      CC plant breeding markers. The recombinant DNA construct is useful for
XX      CC improving plant tolerance to cold, heat, drought, herbicides, extreme
XX      CC osmotic conditions, pathogens or pests, for manipulating growth rate in
XX      CC plant cells by modification of the cell cycle pathway, for conferring
XX      CC increased resistance to plant disease, for producing galactomannan,
XX      CC lignin or plant growth regulators, for increasing the rate of homologous
XX      CC recombination in plants, for improving yield by modification of
XX      CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX      CC or by providing improved plant growth and development under at least one
XX      CC stress condition or for modifying seed oil or protein yield and/or
XX      CC content. This sequence represents a plant full length insert
XX      CC polynucleotide that can be used in the recombinant DNA construct of the
XX      CC invention.
XX      SO Sequence 723 BP; 145 A; 174 C; 198 G; 206 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      5.78e-76      Length:      723
Score:          751.00      Matches:      137
Percent Similarity: 83.0%      Conservative: 48
Best Local Similarity: 61.4%      Mismatches: 38
Query Match:    48.9%      Indels:      0
DB:             13        Gaps:         0

US-10-634-548-2 (1-304) x ADX50931 (1-723)
QY      80 GlyAlaTyrAlaLeuValaLeuSerPheGluSerLeuThrIyArgAnuValIIeGlnGln 99

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Db      7  GGGCGCTACTCTCTTGTGGCGGCTTTGCAGCAGCTCACCGAGCGGCGGCTCATCGAAAG 66
Qy      100 SerLeuSerArgIleValHisIleLeuSerGlyLeuLeuPheValLeuAlaTrpPro 119
Db      67  AGCTTGACGAGAGAGATTGTGACGTCGTCGGCGCTCTGTTTCATATCATCTTGGGCC 126
Qy      120  IlePheSerGlySerThrGluAlaArgIlePheAlaIlePheValProLeuValAsnGly 139
Db      127  CTGTTACAGCAATTCACAGAGACGCTATTTCGCGCGGCTTCCCTTCTCTGAACCTCC 186
Qy      140  LeuArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMetLeuIleLysSerVal 159
Db      187  ATGAGCTTCTGATATGATGACTCCGCTCTACACTGATGAAGCTCTGTAAACACAGTG 246
Qy      160  ThrArgGluGlyArgAlaGluGluLeuLeuGlyGlyProLeuPheTyrValLeuAlaLeu 179
Db      247  ACACTGGAAGAAAACAGAGAAATTGTCGAGAGAGTCCACTTATTAATGTCCTGGTGGC 306
Qy      180  LeuPheSerAlaValPhePheTrpArgIleSerProIleGlyMetIleSerLeuAlaMet 199
Db      307  CTGTTACAGCTTTTACTCTTCTGCGCTGAGTCCCGCATCGGAGATGCTCTCTTGCATG 366
Qy      200  MetCysGlyGlyAspGlyIleAlaAspIleMetGlyArgLysPheGlySerThrIle 219
Db      367  ATGACCGGTGGCGATGTTCCGCTGACATGTTGGAGAGAGGTATGGCTCAGCGAAGCTG 426
Qy      220  ProTyrAsnProArgLysSerTrpAlaGlySerIleSerMetPheIlePheGlyPhePhe 239
Db      427  CCATTCAATCGAGAAAGAGCGGCGCGGAGACATCTCATATTCATTTCTGTTCTCTG 486
Qy      240  IleSerIleAlaLeuTyrTyrIleSerSerLeuGlyTyrLeuHisMetAsnTrpGlu 259
Db      487  CTGTCGCGCATATATATGCTCTACTTCTCAACCTCGGTTATCATGATGTTATCGGGA 546
Qy      260  ThrTrpLeuGlnArgValAlaMetValSerMetValAlaThrValValGluSerLeuPro 279
Db      547  GAGGCACTGTGTAAGCGCGCTGTTGTCATGACGACAGTACGTAGTGGCCCTCTCT 606
Qy      280  IleTrpAspGlnLeuAspAspAsnIleSerValProLeuAlaThrIleLeuAlaIleTyr 299
Db      607  GTGACCGAAGTTGTATGATGACAAATATCTGTTCTTGGCCACCATCTGCTGATGCTTT 666
Qy      300  LeuSerPhe 302
Db      667  CTCTTCTTT 675

RESULT 13
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ID      ADXS1758 standard; cDNA, 753 BP.
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AC      ADXS1758;
XX
DT      21-APR-2005 (first entry)
XX
DE      Plant full length insert polynucleotide seqid 26498.
XX
KW      plant protectant; plant growth regulant; gene therapy; plant;
KW      recombinant DNA construct; physical array; plant breeding marker;
KW      cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW      extreme osmotic condition; pathogen tolerance; pest tolerance;
KW      growth rate; cell cycle pathway; disease resistance;
KW      galactomannan production; lignin production; plant growth regulator;
KW      yield; plant growth; plant development; seed oil; protein yield;
KW      protein content; gene; sb.
XX
OS      unidentified.
XX
PN      US2004034888-A1.
XX
PD      19-FEB-2004.
XX
PF      28-APR-2003; 2003US-00425114.
XX

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PR      06-MAY-1999; 99US-00304517.
PR      05-NOV-2001; 2001US-00985678.
XX
PA      (LIU/J.) LIU J.
PA      (ZHOU/Y.) ZHOU Y.
PA      (KOVA/J.) KOVALIC D K.
PA      (SCRE/J.) SCREEN S E.
PA      (TABAK/J.) TABASKA J E.
PA      (CAO/Y.) CAO Y.
PI      Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
DR      WPI; 2004-180133/17.
XX
PT      New recombinant DNA construct, useful for improving plant tolerance to
PT      cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT      pests, for conferring increased resistance to plant disease, or for
PT      improving yield.
XX
PS      Claim 1; SEQ ID NO 26498; 15bp; English.
XX
CC      The invention describes a recombinant DNA construct comprising a
CC      polynucleotide consisting of a sequence encoding an amino acid sequence
CC      available in electronic form from the US patent office at
CC      ftp://seqdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
CC      of the invention are also useful in physical arrays of molecules and as
CC      plant breeding markers. The recombinant DNA construct is useful for
CC      improving plant tolerance to cold, heat, drought, herbicides, extreme
CC      osmotic conditions, pathogens or pests, for manipulating growth rate in
CC      plant cells by modification of the cell cycle pathway, for conferring
CC      increased resistance to plant disease, for producing galactomannan,
CC      lignin or plant growth regulators, for improving the rate of homologous
CC      recombination in plants, for improving yield by modification of
CC      photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC      or by providing improved plant growth and development under at least one
CC      stress condition or for modifying seed oil or protein yield and/or
CC      content. This sequence represents a plant full length insert
CC      polynucleotide that can be used in the recombinant DNA construct of the
CC      invention.
SQ      Sequence 753 BP; 154 A; 180 C; 206 G; 213 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,14e-76 Length: 753
Score: 751.00 Matches: 137
Percent Similarity: 83.0% Conservative: 48
Best Local Similarity: 61.4% Mismatches: 38
Query Match: 48.9% Indels: 0
DB: 13 Gaps: 0

US-10-634-548-2 (1-304) x ADXS1758 (1-753)
Qy      80  GYAlATYrAlaLeuValLeuSerPheGluSerLeuTrpIleArgAsnValIleGlnIn 99
Db      16  GGGCGCTACTCTTGTGGCGGCTTTGCAGCAGCTCACCGAGCGGCGGCTCATCGAAAG 75
Qy      100  SerLeuSerArgIleValHisIleLeuSerGlyLeuLeuPheValLeuAlaTrpPro 119
Db      76  AGCTTGACGAGAGAGATTGTGACGTCGTCGGCGCTCTGTTTCATATCATCTTGGGCC 135
Qy      120  IlePheSerGlySerThrGluAlaArgIlePheAlaIlePheValProLeuValAsnGly 139
Db      136  CTGTTACAGCAATTCACAGAGACGCTATTTCGCGCGGCTTCCCTTCTCTGAACCTCC 195
Qy      140  LeuArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMetLeuIleLysSerVal 159
Db      196  ATGAGCTTCTGATATGATGACTCCGCTCTACACTGATGAAGCTCTGTAAACACAGTG 255
Qy      160  ThrArgGluGlyArgAlaGluGluLeuLeuGlyGlyProLeuPheTyrValLeuAlaLeu 179
Db      256  ACACTGGAAGAAAACAGAGAAATTGTCGAGAGAGTCCACTTATTAATGTCCTGGTGGC 315
Qy      180  LeuPheSerAlaValPhePheTrpArgIleSerProIleGlyMetIleSerLeuAlaMet 199

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Db 316 CCGTTCAGGCTTTAGTCTTCGGGTAGTCCCATCGGATGCTCTCCCTTCGATG 375
Qy 200 MetCysGlyValAspGlyIleAlaAspIleMetGlyValGlyPheGlySerThrIle 219
Db 376 ATGACCGGGGCGATGCTTCCCTGACATGTTGGAGAGAGGTATGCTCAGCGAAGCTG 435
Qy 220 ProTyrAspProArgLysSerThrPheIleGlySerIleSerMetPheIlePheGlyPhe 239
Db 436 CCATTCATCGAAGAGAGCTGGGCGGAGACATCTGCATCTTCATTTCTGTTCTG 495
Qy 240 IleSerIleAlaLeuLeuTyrTyrTyrSerSerLeuGlyTyrIleHisMetAsnPro 259
Db 496 CTGTCGGGATATGATGCTCTACTCTCAACCTCGGTTATCATGATGTTATCGGAA 555
Qy 260 ThrThrLeuGlnArgValAlaMetValSerMetValAlaThrValValGlnSerLeu 279
Db 556 GAGGACCTGTGTACCTGCGCTTGTTCATCAGCAGCAGCAGTAGTGAGTGCCTTCT 615
Qy 280 IleThrAspGlnLeuAspAspAsnIleSerValProLeuAlaThrIleLeuAlaIle 299
Db 616 GTGACCGAAGTTGTGATGATGACAAATCTGTTCTTGGCCACCATGCTGTACCTTT 675
Qy 300 LeuSerPhe 302
Db 676 CTCTTCTT 684

RESULT 14
ADXS1714
ID ADXS1714 standard; cDNA, 937 BP.
XX
AC ADXS1714;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 26454.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomanan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
XX
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
DR WPI: 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX

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PS Claim 1, SEQ ID NO 26454; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomanan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
SQ Sequence 937 BP; 167 A; 261 C; 277 G; 232 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 9.17e-75 Length: 937
Score: 742.00 Matches: 152
Percent Similarity: 72.88 Conservative: 57
Best Local Similarity: 53.04 Mismatches: 62
Query Match: 48.34 Indels: 17
DB: 13 Gaps: 4
US-10-634-548-2 (1-304) x ADXS1714 (1-937)
Qy 29 SerProGlyPheLeuIle-----SerSerProCysPheIleGlyLeuThr--Gly 44
Db 34 TCCCCCACTGCGTCTGCTCTCGCGCTCGCTCCCGCCGCGCGCTGCGCTTCG 93
Qy 45 MetGlySerAlaThrGlnLeuArgAlaArgPheSerLeuIleSer-----59
Db 94 CTGGAGAGCTCCATGCGG-----AGGGGCTCTCTGCTGCGCGTCCGACGCCCGGCC 144
Qy 60 -----SerAlaValAlaIleThrAsnSerLeuHisAspValGlyAlaThrVal 75
Db 145 GTGGCGGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTG 204
Qy 76 AlaValLeuGlyGlyAlaTyrAlaLeuValLeuSerPheGlnSerLeuThrLysArgAsn 95
Db 205 CTCATCACCGCGCGCGCTTACTCTTGTGCGCGCTTCAGACGAGCTCACGAGCGGCGG 264
Qy 96 ValIleGlnGlnSerLeuSerArgLysLeuValHisIleLeuSerGlyLeuLeuPheVal 115
Db 265 CTCATCGAAGAGAGCTTGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 324
Qy 116 LeuAlaTyrProIlePheSerGlySerThrGlnAlaArgTyrPheAlaAlaPheValPro 135
Db 325 TCATCTTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 384
Qy 136 LeuValaGlnGlyLeuArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMetLeu 155
Db 385 TTCCTGAATCTCAGAGAGCTTCTGATATATGAGACTCCGCTCTACATGATGAGAGCTCTG 444
Qy 156 IleLysSerValIleThrArgGlnGlyValArgAlaGlnGlnLeuLeuValGlyProLeuPhe 175
Db 445 GTAAATATGAGACACCGGAGAGAAACCAAGAGAAATGCTGAGAGG-CCACTCTATTAT 503
Qy 176 ValLeuAlaLeuLeuPheSerAlaValPhePheThrArgGlnSerProIleGlyMetIle 195
Db 504 GTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 563
Qy 196 SerLeuAlaMetMetCysGlyValAspGlyIleAlaAspIleMetGlyValGlyPheGly 215
Db 564 TCCTTTCATGATGAGAGAGCGGTGCGATGTTCCCTGACATGTTGGAGAGAGATATGCG 623

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Alignment Scores:

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100-443687

Score:

648.00
100.00

Matches: 1

Best Local Similarity: 100.0
 Query: Match: 43.3%

Mismatches: 0

DB: 3

Gaps: 0

US-10-634-548-2 (1-304) X AAC53042 (1-494)

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21 SerLeuThrThrHisArgpneCysserProglypneLeuIeserSerProCyspneIle 40

Db 168 TCTTTGACGACTCACC GGTTCTGTTCTCTCC TGGCTTCTTGATTCTTCTCTCCTTGTTCATT 227

41 GlyLeuThrGlyMetGlySerAlaThrGlnLeuArgAlaArgArgSerLeuIleSerSer 60

228 GGTTCACCGAATGGGCTCTGCTACTCAGTTACGTGCTCGTCGTTCTCTGATCTCTCA 287

61 AlavAlaIatHrrAsnSerLeuLeuHisAspValGlyAlaThrValAlaValLeuGlyGly 80

Db 288 GCAGTTGCACGAATTCGCTGTTGCATGACGTCGGAGCCACCCTGGCAGTSCCTTGGTGA 347

81 AlaTyrAlaLeuValLeuSerPheGluSerLeuThrLysArgAsnValIleGlnGlnSer 100

Db 348 GCATACGCGCTTGTCTTAAGCTTCGAGAGTCTCACCAGCGAAACGTCATTCAACAGAGT 407

101. LeuSerArgLySLeuValHisIleLeuSerGlyLeuLeupheValLeuAlaTrpProIle 120

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QY 121 pneserGlyserThrcIuaIaargTyr 129

D_b 468 TTCAGCGGATCGACCGAGGCTCGATAC 494

Search completed: March 15 2006 20:05:26

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ALIGNMENTS

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	REFERENCE	
	AUTHORS	
	TITLE	
	JOURNAL	
	COMMENT	
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	Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Setou,M., Nakajima,M.,	
	Atiyama,K., Enyu,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,	
	Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A.,	
	Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.	
	Large scale analysis of Arabidopsis full-length cDNA	
	Unpublished (2002)	
	Contact: Motoaki Seki	
	Plant Functional Genomics Research Group	
	Riken Genomic Sciences Center	
	3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan	
	Tel: 81-298-36-4359	
	Fax: 81-298-36-9060	
	Email: msek@rc.riken.go.jp	
	An Arabidopsis full-length cDNA library was constructed essentially	
	as reported previously (Seki et al., 1998). cDNA cleaved with BamHI	
	and XhoI was ligated to modified Lambda Pfu-I vector (Carninci et	
	al., submitted for publication) digested with BamHI and SalI. This	

clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plan/index_e.html) for further details.

FEATURES

source

Location/Qualifiers

1. 636
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/clone_1ib="RAFL15"
/note="Site_1: BamHI; Site_2: SalI"

ORIGIN

Alignment Scores:

Pred. No.:	6.8e-95	Length:	636
Score:	924.00	Matches:	185
Percent Similarity:	97.94	Conservative:	0
Best Local Similarity:	97.94	Mismatches:	4
Query Match:	60.24	Indels:	0
DB:	1	Gaps:	0

US-10-634-548-2 (1-304) x AU236980 (1-636)

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DB 70 ATGGAGCAACCTTACCTTATCTCCGACATCAATCAAGTGTGTGGTCCGAGCAAC 129
QY 21 SerLeuThrThrHisArgPheCySerProGlyPheLeuLeuSerSerProCyPheIle 40
DB 130 TCTTGAAGACCTCAACGGGTCTGCTCTGCGCTTCTGATTTCTTCTCTGTTTCAAT 189
QY 41 GlyLeuThrGlyMetGlySerAlaThrGlnLeuAlaArgArgSerLeuIleSerSer 60
DB 190 GGTGTGACCGGAAATGGGCTGCTACTCACTACGATACGTCGTCGTCCTGATCTTCA 249
QY 61 AlaValAlaIleThrAsnSerLeuLeuHisAspValGlyAlaThrValAlaValLeuGly 80
DB 250 GAGTTGGACGCAATTCGCTGTGTGATGAGTCGAGGCCGCGTGGCACTGTTGGTGA 309
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DB 310 GCATACGGCTGTCTTAAGCTTCGAGAGTCTCACCAAGCGAAAGTATTCAACAGAGT 369
QY 101 LeuSerArgLeuValHisIleLeuSerGlyLeuLeuPheValLeuAlaTrpProIle 120
DB 370 TTGACGACAAAGCTTGTGATATACCTCAAGCTGCTTTTCTGACTTGGCGCAATC 429
QY 121 PheSerGlySerThrGlnAlaArgTyrPheAlaIlePheValProLeuValAsnGlyLeu 140
DB 430 TTCACGGAGTCACGAGGCTCGATACCTTGTGCTTTTGTCCGTTAGTGAATGGCTTA 489
QY 141 ArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMetLeuIleIleSerValThr 160
DB 490 AGCGTTGTTATTAAGCACTATCCATTCCCAAAATGCATCTAATATCCGTCACA 549
QY 161 ArgGlyGlyArgAlaGlnGlyLeuLeuLeuGlyProLeuPheTyrValLeuAlaLeuLeu 180
DB 550 AAGAGAGGAGAGAGAGAGAGTGTCTTAAGGTCCTTGTGTCATGCTTACTCTTCT 609
QY 181 PheSerAlaValPhePheTrpArgIle 189
DB 610 TTCTCTGCGGANTTTCTTCTGAGAGAG 636

RESULT 2

DR914339/c

864 bp mRNA linear EST 02-AUG-2005

DEFINITION EST1105878 Aquilegia cDNA library Aquilegia formosa x Aquilegia

pubescens cDNA clone COL102, mRNA sequence.

ACCESSION DR914339

VERSION DR914339.1 GI:71683702

KEYWORDS EST.

SOURCE

ORGANISM

Aquilegia formosa x Aquilegia pubescens
Aquilegia formosa x Aquilegia pubescens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Ranunculaceae; Aquilegia.

REFERENCE

1 (bases 1 to 864)

AUTHORS

Hodges, S.A., Remsink, W., Buell, C.R., Borevitz, J., Kramer, E.,
Nordborg, M. and Tomkins, J.

TITLE

Generation of ESTs from Aquilegia

COMMENT

Unpublished (2005)

Other ESTs: EST1105879

Contact: Scott Hodges

Department of Ecology, Evolution and Marine Biology

University of California, Santa Barbara

Santa Barbara, CA 93106, USA

Tel: 805 893 7813

Fax: 805 893 4724

Email: hodges@lifesci.ucsb.edu

Seq primer: TTTTCTTTTCTTTTCTTTT (where N = A, G & C).

FEATURES

source

Location/Qualifiers

1. 864
/organism="Aquilegia formosa x Aquilegia pubescens"
/mol_type="mRNA"
/db_xref="taxon:338618"
/clone="COL102"
/tissue_type="mixed shoot and floral apical meristems,
flower buds, leaves and roots"
/lab_host="DH10B T1 (T1 and T5 phage resistance)"
/clone_1ib="Aquilegia cDNA library"
/note="Vector: pCMV SPORT6.1; Site_1: EcoRI, Site_2: NotI;
F2, F3, and F4 lines of Aquilegia formosa x A. pubescens
were grown from seed in greenhouses at UC Santa Barbara.
From these plants three sets of tissue were collected: 1)
Small flower buds (<10 mm) and very young inflorescences
(71 & 29% by weight respectively), 2) Medium (7-20 mm) and
large (at or near anthesis) flower buds (65 & 35% by
weight respectively) and 3) Shoot apical meristems. A
fourth set of tissue was collected from plants of A.
formosa. These plants were grown from seed in sand and at
approximately 1 month root tissue and leaf tissue of
various developmental stages were collected (84 & 16% by
weight respectively). Total RNA was extracted from each
set of tissue and pooled in the following proportions:
1.5x from sets 1 & 2, 1x from sets 3 & 4. From the pooled
total RNA, mRNA was extracted and enriched for full-length
messages and then normalized with proprietary methods by
Invitrogen."

ORIGIN

Alignment Scores:

Pred. No.:	8.31e-84	Length:	864
Score:	829.00 <td>Matches:</td> <td>156</td>	Matches:	156
Percent Similarity:	82.28 <td>Conservative:</td> <td>47</td>	Conservative:	47
Best Local Similarity:	63.28 <td>Mismatches:</td> <td>44</td>	Mismatches:	44
Query Match:	54.04 <td>Indels:</td> <td>0</td>	Indels:	0
DB:	8	Gaps:	0

US-10-634-548-2 (1-304) x DR914339 (1-864)

QY 58 ILeSerSerAlaValAlaIleThrAsnSerLeuLeuHisAspValGlyAlaThrValAlaVal 77
DB 816 ATATTAGATTCACATCGCAACGCGCACCTTGGCAGATGACGAGCGCGGACACTTGT 757
QY 78 LeuGlyGlyAlaTyrAlaLeuValLeuSerPheGlySerLeuThrIleArgAsnValIle 97
DB 756 AGTGTGTGCTTACTGTTGTATGCTTTCTTGAATCTTAAGTGAAGGAAATTTAAATC 697
QY 98 GlnGlnSerLeuSerArgLeuValHisIleLeuSerGlyLeuLeuPheValLeuAla 117
DB 696 AAACGAGTTTACGACGAAAGTGTTCATATTTGTCTGCTCTTATTCATGCTTCT 637
QY 118 TrpProIlePheSerGlySerThrGlnAlaArgTyrPheAlaIlePheValProLeuVal 137

Db		636	TGGGCAATTTTAGTAACTCACAAGCGAAGTGCCTACTTGTCGTGATTGTCCTCTTTGG	577
Oy		138	AenqglyLeuArgLeuValIleasnGLyleuSerIIeserProAsnSermethLeuIleyls	157
Db		576	AATGCTTGAGGCTGTCTCCTCATAGCACTTTCACAGACCTGAAGAGGCTTCCTGAAA	517
Oy		158	SerValIThrArgSLingLYlArghlaIngluLenuleuLySGlyProLeuPheThrFallen	177
Db		516	TCGTGCACACGGAGAGAAATCCAAAGAAGACTTCGAGAGGCTCTCTACTACAGTTCTCA	457
Oy		178	AlaLeuLeuPheSerAlaValPhePheThrParGluSerProIleGlyMetIIeserLeu	197
Db		456	ATGTTGATTGCCAGTCAGCACTACTATTTCGGCGTGAATCTCCAGCTGGAGATGATTGCACA	397
Oy		198	AlaMetMetCyegLYGLYAspGLYLlealaaspIIemetGLYArgLYasPheGlySerThr	217
Db		396	GCTAAGATGATGTGGTGGGAGATGGTTTTGCTGATATCATTTGGAAGAAGATTGGGTCACTA	337
Oy		218	LYslleProTYrAsnProArglysSerTrpAlaglyserIIeserMetPheIIephely	237
Db		336	AAGATCCCATAATTAATCAAAAAAGATTGATGGTGAAGTTCTCCATGTTCTATTTTGAT	277
Oy		238	PhePheIIeserIIeAlaleuLeuTyTYTYTYrSerSerLeuGLYrIleuHImetAsn	257
Db		276	TTCTTGTTCTCAATCATATGTTGCTATACATTTTTTCAGCTCTTGATTTTCCAATTGGAC	217
Oy		258	TrpGluThrThrLeuGlnArgValAlaMetValSerMetValAlaThrValAlaGluSer	277
Db		216	TGGTCATCATCAGTGGGANAAGTGGCTTTAGTACGCTTGAGCTTGCAACCATAGTGAATCC	157
Oy		278	LeuProIleThrAspGlnLeuAspAspAsnIIeserValProLeuAlaThrIleuAla	297
Db		156	CTTCTACTACAGAAATGTAGATATACAAACATMACTGTTCCATTATCCAGCATGCTAATG	97
Oy		298	AlaTYrLeuSerPheGLYTYr 304	
Db		96	GCATTATGTTTTCAGCTAT 76	
RESULT 3				
LOCUS	CB261126	524 bp	mRNA	linear EST 06-NOV-2003
DEFINITION	26-B9406-012-002-C04-c7r MP1Z-ADIS-012 Arabidopsis thaliana cDNA			
VERSION	CB261126			
KEYWORDS	CB261126.1 GI:32885899			
SOURCE	EST.			
ORGANISM	Arabidopsis thaliana (chale crese)			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsits.			
REFERENCE	1 (bases 1 to 524)			
AUTHORS	Schmid,K.J., Soerenen,T.R., Stracke,R., Torjek,O., Altmann,T., Mitchell-Olds,T. and Weisshaar,B.			
TITLE	Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana			
JOURNAL PUBMED	Genome Res. 13 (6), 1250-1257 (2003) 12799357			
COMMENT	Contact: Weisshaar B ADIS DNA core facility at MPIZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851 Email: weisshaar@mpi-z-koeln.mpg.de Insert Length: 524 Scd Error: 0.00 Plate: 2 row: C column: 04 Seq primer: T7R; CTATACGACTCTATAGGA. Location:Qualifiers 1..524 /organism="Arabidopsis thaliana" /mol_type="mRNA" /ecotype="landberg erecta" /db_xref="GABI:589752"			
FEATURES	Source			

	<pre> /db xref="taxon:3702" /clone="MP12p79C0420" /tissue_type="whole plant" /dev stage="adult plant, mixed stresses" /lab host="E. coli XL1-Blue MRF" /clone_lib="MP12-ADIS-012" /notes="vector: pSPORI; Site 1: SalI; Site 2: NotI. cDNA library from Arabidopsis thaliana, accession Landberg erecta; six weeks old total plants grown under long-day conditions in soil, whole adult plants were treated for 24 hours with different stresses, (1) at 4M-0 C in the dark, (2), at 37 Grad C in the dark, (3) lying in the lab after removing from soil, (4) in the greenhouse after wounding leaves with a foreceps, (5) in the lab watering with a 150 mM NaCl solution, (6) at 26 Grad C in the light/UV; equal quantities of stressed plant material were pooled; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites SalI-NotI, primer sites and orientation: T7-salI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-SP6. Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection', PI: Bernd Weisshar. Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de. This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information." </pre>		
ORIGIN			
Alignment Scores:			
Pred. No.:	7,13e-79	Length:	524
Score:	783,00	Matches:	157
Percent Similarity:	100,0%	Conservative:	0
Best Local Similarity:	100,0%	Mismatches:	0
Query Match:	51,0%	Indels:	0
Db:	6	Gaps:	0

US-10-634-548-2 (1-304) x CB261126 (1-524)			
QY	1	Meta1a1a1aThrLeuPProLeuSerProIleAsnHisGlnLeuCyAArgPheG1YAspAsn	20
DB	52	ATGGGAGCAACTTAACCTTAATCTTCCGATCATATCATGTTGTTCGGTTCCGGAAACAC	111
QY	21	SeirLeuThrThiHisAArgPheCyASeSerProG1YPheLeuIleSeSerProCyAphel1e	40
DB	112	TCTTTAGCAATCAACCGGTTCTGTCTTCCTCGCTTCTTGATTCTTCTCCGTGTTCAAT	171
QY	41	G1YLeuThrG1YMetG1YSerAlaTh-G1nLeuArgAlaArgAysSerLeuIleSerSer	60
DB	172	GGTTTGAACCGGAAGGGCTCTGCACTACAGTACAGTACGCTCGCTCTCTGATCTCTTCA	231
QY	61	AlaValAlaThrAsnSerLeuLeuHisAspValG1YAlaThrValAlaValLeuG1YG1Y	80
DB	232	GCAGTTGGAGCAAAATTCGCTGTGTGCATGACCTCGAGCCACCCGCGGACGCTTG7GGA	291
QY	81	AlaTyra1aLeuValLeuSerPheG1YSerLeuThrTyAArgAsnVal1leG1nG1nSer	100
DB	292	GCAATCCGCGCTTGTCTTAAAGTTGGAAGTCTCCACAGCAAGCAACGTCATTCAACAAGT	351
QY	101	LeuSerArg1YLeuValHis1leLeuSerG1YLeuLeuPheValLeuAlaTrpPro1le	120
DB	352	TTGAGCAGAAAGCTTGGCATATATCTCTCAAGGTCGTGCTTTTCGTAATTCGCGCCATTC	411
QY	121	PheSerG1YSerThrG1YAlaArgTyTPheAlaAlaPheValPProLeuValAsnG1YLeu	140
DB	412	TTTCAGCGAATCGACCGAGGCTCGAATATTTGGCTTTTGTTCGTAAGGAAGGCTTAA	471
QY	141	ArgLeuVal1leAsnG1YLeuSer1leSerProAsnSerMetLeu1le1Ys	157
DB	472	AGGCTTGTATTAAACGACTATTCATTTCGCCAAATTCGATGCTAAACAA	522

RESULT 4	
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CK286787 881 bp mRNA linear EST 02-AUG-2004
 LOCUS CK286787
 DEFINITION Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NEMB462 5' end, mRNA sequence.
 ACCESSION CK286787.1 GI:39862689
 VERSION CK286787
 KEYWORDS EST.
 SOURCE Nicotiana benthamiana
 ORGANISM Nicotiana benthamiana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.
 REFERENCE 1 (bases 1 to 881)
 AUTHORS Buell, C.R., Hart, A., Zisemann, V., Karimicheva, S.A., Day, B., Staskiewicz, B., Jin, H. and Baker, B.
 TITLE Generation of EST sequences from Nicotiana benthamiana
 JOURNAL Unpublished (2003)
 COMMENT Other ESTs: EST749510
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from the University of Arizona Genomics Institute via http://genome.arizona.edu/orders/
 Seq primer: ATT TAG GTG ACA CTA TAG.
 FEATURES
 source
 location/Qualifiers
 1..881
 /organism="Nicotiana benthamiana"
 /mol_type="mRNA"
 /db_xref="taxon:4100"
 /clone="NEMB462"
 /tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"
 /lab_host="DH10B-Tona"
 /clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"
 /note="Vector: pCMVSPORT.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv. tomato 12 hr; Pseudomonas campestris pv. campestris 12 hr, 18hr; Pseudomonas syringae pv. phaseolicola 18hr, and Pseudomonas campestris pv. vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,15e-77 Length: 881
 Score: 775.50 Matches: 150
 Percent Similarity: 73.3% Conservative: 43
 Best Local Similarity: 57.8% Mismatches: 51
 Query Match: 50.5% Indels: 23
 Gaps: 5
 US-10-634-548-2 (1-304) x CK286787 (1-881)
 QY 16 ArgpHeGlyAsn-----AsnSerLeuThrThrHis----- 25
 DB 82 CGTTTCTGGAATCGCTTCCTCTCTCACTGATACCCACACTTACATTGCGCGA 141
 QY 26 ArgpHeCysSerPro-----GlyPheLeuIleSerSerProCysPheIleGlyLeuThr 43
 DB 142 CCAATTCCTCCGCCGACAGTTCCCGAGCGTTCCTGCTGCGCCGACCGCGTTTAA 201
 QY 44 GlyMetGlySerAlaThrGlnLeuArgAlaArgArgSerLeuIleSerSerAlaValAla 63
 DB 202 GGTTGGTTTGATGCT-----ATAATTGGAGATGCC----- 231
 QY 64 ThrAsnSerLeuHisAspValGlyAlaThrValAlaValLeuGlyGlyAlaTyrAla 83

DB 232 ---GGCTCAGTGTGACAGATGCGGAGCCACGGCTTGGTCATCGCTGATCC 288
 QY 84 LeuValIleSerPheGlySerLeuThrLysArgenValIleGlnInSerLeuSerArg 103
 DB 289 CTGTTCCTCACTTTCGATTTCTTATCCGAGCGCAAGCTCATTTACATTTTAA 348
 QY 104 LysLeuValHisIleLeuSerGlyLeuLeuPheValLeuAlaTyrProIlePheSerGly 123
 DB 349 AAGCTTGGCCACATTTGTCTGTCTGTTTATGCTTCTGCGCAATTTTACGCA 408
 QY 124 SerThrGlnAlaArgTyrPheAlaAlaPheValProLeuValAlaGlyLeuArgLeuVal 143
 DB 409 TCAAGATGGGACCGCTACTTGTCTGTAGTTCGCTTACAACTGTTTGAAGCTTGTG 468
 QY 144 IleLeuGlyLeuSerIleSerProAsnSerMetLeuIleLysSerValThrArgGlyGly 163
 DB 469 ATTATGCGCTTTCCTTGGCTACTGATGAGGAGCTCTTAAATCTGTACTCGGAGGA 528
 QY 164 ArgAlaGlyGlyLeuLeuLeuGlyProLeuPheTyrValLeuAlaLeuLeuPheSerAla 183
 DB 529 AAGCCAGAGAAATTTGCTTAGAGGCGCTTATATATGTTATGTTAATTGACCGCA 588
 QY 184 ValPhePheTyrPArgLysSerProIleGlyMetIleSerLeuAlaMetMetCysGlyGly 203
 DB 589 CTTCCTTTTGGCGTGAATCACAGATTGAGACTAATTCGTTAGCAATGATGTGTGTGT 648
 QY 204 AepGlyIleAlaAplIleMetGlyArgLysPheGlySerThrLysIleProTyrAsnPro 223
 DB 649 GATGGAATTCGTGATATGTTGGAAGAGTTGGCTCATRAAAATCCCTTATATAA 708
 QY 709 CAGAAATTTGGCTGTGATGAGCTCTCCATGTTTGTCCGTTTCTGTGATGATGCGG 768
 QY 244 LeuLeuTyrTyrTyrSerSerLeuGlyTyrLeuHisMetAsnTyrGlnThrThrLeuGln 263
 DB 769 ATGCTCTTATCTTCTCTCCCTTGGAGATCTTCACTTGAGTTGGTTCAACTTA 828
 QY 264 ArgValAlaMetValSerMetValAlaThrValAlaGlySerLeuProIle 280
 DB 829 AGTGAAGCTGTGGGTCTATTATACCACTATGTTGAGTCTTACTTATTT 879
 RESULT 5
 CO981750/c 650 bp mRNA linear EST 13-SEP-2004
 LOCUS GM89012A2C07.r1 Gm-r1089 Glycine max cDNA clone Gm-r1089-4334 3,
 DEFINITION mRNA sequence.
 ACCESSION CO981750
 VERSION CO981750.1 GI:51337884
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max (soybean)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 REFERENCE 1 (bases 1 to 650)
 AUTHORS Vodka, L., Shoemaker, R., Keim, P., Polacco, J.C., Retzel, E., Khanna, A., Snealy, R., Clough, S., Thibaud-Nissen, F., Correll, V., Erbe, J., Gonzalez, D.O., Stromov, M., Rodriguez-Huete, A.M., Schweitzer, P., Gong, G. and Liu, L.
 TITLE A Functional Genomics Program for Soybean (NSF 9872565) (2004)
 JOURNAL Unpublished (2004)
 COMMENT Other ESTs: BQ252454 corresponding to Gm-cl052-5684 (5')
 Contact: Vodka, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
 Lewin, H. A., Director, Keck Center for Comparative and Functional Genomics
 University of Illinois
 Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
 Tel: (217) 244-6147
 Fax: (217) 333-4582

Email: l-vodkin@iuc.edu
 Plate: GM69012A2 row: C column: 07
 Seq primer: 5'-TTTTTTTTTTTTTTTTT(A/C/G)-3'
 High quality sequence ecop: 650.
 Location/Qualifiers

FEATURES

Source

1..650
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="Gm-r1089-4334"
 /clone_11b="Gm-r1089"
 /note="The library Gm-r1089 is a sequence-driven, reracked set of 9,216 low redundancy clones selected from 38 different cDNA libraries constructed from various tissues and stages of development of soybean including 973 cDNAs from germinating cotyledons (source library Gm-c1069, Gm-c1076, and Gm-c1077); 1,465 cDNAs from various tissue and organ systems of the adult plant; 476 cDNAs from adult stem tissue (source library Gm-c1062); 1340 cDNAs from tissue culture derived somatic embryos (source libraries Gm-c1036 and Gm-c1075); 2918 cDNAs from hypocotyls or young seedlings; 742 cDNAs from germinating seedlings, shoot tips, or leaves exposed to various stresses (source libraries Gm-c1065, Gm-c1066, and Gm-c1068); 839 cDNAs from young leaves or hypocotyls exposed to bacterial and fungal pathogens (source libraries Gm-c1072, Gm-c1073, Gm-c1074, and Gm-c1084); and 463 from roots of young plants grown in hydroponic media without phosphate (source library Gm-c1087). The 5' ESTs of the source clones from the different libraries were used to select singletons, or a representative of each contig, which were reracked to form library Gm-r1089 and the cDNA clones of the reracked Gm-r1089 library were then sequenced at the 3' end. The plant genome project #9872565
 (http://soybean.genomics.croplsci.uiuc.edu/) as part of creation of a low redundancy soybean cDNA set. The source cDNA libraries were constructed by the laboratories of Lila Vodkin, University of Illinois, Randy Shoemaker, Iowa State University, and Paul Keim, Northern Arizona University as part of the Public EST project, http://129.186.26.94/soybeanest.html. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://web.ahc.umn.edu/biodata/nstoy/. Reracking and 3' sequencing were conducted by services of the University of Illinois Keck Center for Comparative and Functional Genomics http://www.biotech.uiuc.edu/keck.htm. Note: The corresponding 5' EST from each clone in the Gm-r1089 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the clone ID of the original cDNA library that is also listed under 'OTHER EST'."

ORIGIN

Alignment Scores:

Pred. No.: 8.81e-77 Length: 650
 Score: 766.00 Matches: 145
 Percent Similarity: 84.9% Conservative: 35
 Best Local Similarity: 68.4% Mismatches: 32
 Query Match: 49.9% Indels: 0
 DB: 7 Gaps: 0

US-10-634-548-2 (1-304) x CO981750 (1-650)

QY 91 LeuThlyARcGAsnValIleGInGInserLeuSerArglyLeuValHisIleLeuSer 110
 DB 645 CTCACCTCGAGAAACATCTCCAAACAGGCTCTGACGAGAAACCTGCTCATATATTAATCT 586
 QY 111 GlyLeuLeuPheValIleuAlaTrpProIlePheSerGlySerThrGluAlaArgTyrPhe 130
 DB 585 GGCTTGCTTTTCTGCTTCTGCTGCTATTTTCAGCAACTCCCTTAAGGCTCGTACTTCTT 526

FEATURES

Source

QY 131 AlaAlaPheValProLeuValAsnGlyLeuArgLeuValIleAsnGlyLeuSerIleSer 150
 DB 525 GGCGCTTTGTTGCTCTGCTGCAATGCTTGAGGCTTTGGTCAAGGCTCTCAGCTGCT 466
 QY 151 ProAnserMetLeuIleLeuSerValThrArgGluGlyArgAlaGluGluLeuLeuLys 170
 DB 465 TGTATGAGGAGCATCATCAATCCGTCCAGAGAGAGAGATCCATGAATGCTAAGG 406
 QY 171 GlyProLeuPheTyrValIleuAlaLeuLeuPheSerAlaValPhePheTyrArgGluSer 190
 DB 405 GGTCCCTTTTATGTTGCTGATCTGATTTATCTGCTGCTGCTGCTGCTGCTGCTGCT 346
 QY 191 ProIleGlyMetIleSerLeuAlaMetMetCysGlyGlyArgPylIleAlaAspIleMet 210
 DB 345 CCAATGTGTGATCTCTCTGCAATGATGATGATGATGATGATGATGATGATGATGAT 286
 QY 211 GlyArgLysPheGlySerThrLysIleProTyrAsnProArgLysSerTyrAlaGlySer 230
 DB 285 GGTAGAAATATATGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 226
 QY 221 IleSerMetPheIlePheGlyPhePheIleSerIleAlaLeuLeuTyrTyrIleSer 250
 DB 225 ATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 166
 QY 251 LeuGlyTyrLeuHisMetAsnTyrGluThrThrLeuGluAlaGlyValAlaMetValSerMet 270
 DB 165 TTAGCAATGTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 106
 QY 271 ValAlaThrValAlaGluSerLeuProIleThrArgGlnLeuAspAsnIleSerVal 290
 DB 105 GTGGCAATATGTCGTGATGCTCTTCCCATTTACTAAGTAGAGTAGAGTAGAGTAGAG 46
 QY 291 ProLeuAlaThrIleLeuAlaAlaTyrLeuSerPhe 302
 DB 45 CCACAGCTACCAAGGACAGTGGCATTTTTCACCTTC 10

RESULT 6
 LOCUS CV711742/c 883 bp mRNA linear EST 03-NOV-2004
 DEFINITION UCRPT01_001605.f Poncirtus trifoliata CTV-challenged cDNA library -
 AG12 Poncirtus trifoliata cDNA clone PT_65A001605, mRNA sequence.
 ACCESSION CV711742
 VERSION CV711742.1 GI:55294110
 KEYWORDS EST.
 SOURCE Poncirtus trifoliata
 ORGANISM Poncirtus trifoliata
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosoids; eurosids II; Sapindales; Rutaceae; Poncirtus.
 REFERENCE 1 (bases 1 to 883)
 Roose, M.L., Ye, X., Federici, C.F., Close, T.J., Fenton, R.D.,
 Wamamaker, S., Kim, H.R., Kudrna, D. and Stum, D., Misoski, M.,
 Wing, R.
 Development of EST Resources and New Genetic Markers for California
 Citrus - Poncirtus trifoliata CTV-challenged phloem - AG12
 Unpublished (2004)
 CONTACT: Mikeal Roose
 Department of Botany & Plant Sciences, University of California
 Riverside, CA, 92521-0124, USA
 Tel: 9097874137
 Fax: 9097874437
 Email: mikeal.roose@ucr.edu
 Seq primer: 77.
 Location/Qualifiers
 1..883
 /organism="Poncirtus trifoliata"
 /mol_type="mRNA"
 /cultivar="Pomeroy OP"
 /db_xref="taxon:37690"
 /clone="PT_65A001605"
 /tissue_type="Phloem"
 /dev_stage="10 - 30 cm shoots"

US-10-634-548-2 (1-304) X CV711742 (1-883)

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Oy 97 ILeGlnGlnSerLeuSerArgLybLeuValhSllLeuSerGlyLeuLeuPheValLeu 116
      : : : : :
Db 880 TTGGAAcAGGTTTAAAGCAAAAACTGTACATATATTGTGGGAGTTGTATTATCATGAGTT 821
Oy 117 AlaTrpProIlePhe----- 121
      : : : : :
Db 820 TCATGGCCAAATTTTCAGGTTCCCTCGGTATATGAAATTTTAAcAAATTCAGTTGT 761
Oy 122 -----Ser 122
      : : : : :
Db 760 TTGTATATTGCGTGCGTTTCTTAACTTTCAATCATATTATTGAATACATATATAGC 701
Oy 123 GlySerThiGluAlaArgLyPheAlaAlaPheValProLeuValaSerGlyLeuArgLeu 142
Db 700 ACCCAACAAGAGCGCTGCTACTTGTGCGGCTTGTGTCCTGTGGAAATTCGTTAGACTT 641
Oy 143 ValIleasnLyLeuSerLleSerProAsnSerMetLeuLleLeuSerValThrArgGlu 162
      : : : : :
Db 640 GTCAATTACGCGCCTTCATTATTAAGTAAGATGGGCTATATAAAATCTGTACTCGTGA 581
Oy 163 GlyArgAlaGlnGlnLeuLeuLysGlyProLeuPheYrValLeuAlaLeuLeuPheSer 182
      : : : : :
Db 580 GGAACACCAACCAAGAGATTGCTTAAGGGCCATTATATATAGTCTGTATATATCTTCT 521
Oy 183 AlaValaPhehetrPArgGlnSerProIleGlyMetLleSerLeuAlaMetMetCysGly 207
      : : : : :
Db 520 GCTCTTGTCTTTTGGCGGTGATTCGACAGTTGGGGTGATCTCTCTCATGATGTGTGGG 461
Oy 203 GlyPheGlyLleAlaAspLleMetGlyArgLybPheGlySerThryLleIleProGlyAsn 222
      : : : : :

```

FEATURES
SOURCE

```

/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCCSD2C02H02"
/lab_host="DH10B"
/clone_lib="SD2"
/notes="Organ: Developing seeds (small insert library);
Vector: pSport1, Site 1: SalI, Site 2: NotI; An
undirectional cDNA library generated from [developing
seeds (small insert library)]. cDNA was prepared from
poly(A+ mRNA using Superscript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a agarose gel. 2-8 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucst.tad.tc.utdcamp.br/public"

```

ORIGIN

Alignment Scores:

Pred. No.:	1,27e-75	Length:	78
Score:	757.00	Matches:	13
Percent Similarity:	81.4%	Conservative:	49
Best Local Similarity:	59.4%	Mismatches:	43
Query Match:	49.3%	Indels:	0
DB:	6	Gaps:	0

US-10-634-548-2 (1-304) X CA297624 (1-787)

Qy	74	ThrValAlaValLeuGlyValAlaTyralaLeuValLeuSerPheGlySerThrIleuTyrs	93
Db	776	ACGGGCTCATCATCGTGGCCGACNCTCTTTGTGGGGTCTTCGACGAGCTCACGGAG	717
Qy	94	ArgAsnValIleGlnGlnSerLeuSerArgIysLeuValHisIleLeuSerGlyLeuLeu	113
Db	716	CGGCGAGCTCATGTGAAMAAGTTTGAGCAGGAAGNCTGTGCATCTGTATCTGGCGTCTG	657
Qy	114	PheValLeuAlaIleTyrProIlePheSerGlySerThrGlnAlaArgTyrPheAlaIlePhe	133
Db	656	TTCAATCATCTTGGCCACTGTTCAGTAATTCGACGAAAGCAGGTAATTCGCCCGCAGTT	597
Qy	134	ValProLeuValAsnGlyLeuArgLeuValIleAsnGlyLeuSerIleSerProAsnSer	153
Db	596	GTTCCATCTCTTGAACTCCATTAAGCTTTCGACATACGCACTCCGGCTTACACTGATGAA	537
Qy	154	MetLeuIleIysSerValIleThrArgGlnIysArgAlaGlnGlnLeuLeuIysGlyProLeu	173
Db	536	GCTTCAGTAATAATCAAGTGAACGCTGAAGAAACACAGAGAAATTACTGAAGAGTCCACTC	477
Qy	174	PheTyrValIleuAlaLeuLeuPheSerAlaValPhePheTyrArgIleuSerProIleGly	193
Db	476	TATATATGCTTGCTGCTGCTGTTCAAGTGTATTAGTCTTCGGGGTGAGTCCCCCATTTGGG	417
Qy	194	MetIleSerLeuAlaMetMetCysGlyValSerGlyIleAlaAspIleMetGlyArgIys	213
Db	416	ATTGATATCTTGTCATGATGATGAGTGGTGCATGTTTGCTGACATTTGTGGGAAGAAG	357
Qy	214	PheGlySerThrIleGlyIleProTyrAsnProArgIysSerThrAlaGlySerIleSerMet	233
Db	356	TATGGCTCAGTGAACCTGCCATTCAATGAGAAGAAGATTTGGCCCGGAAGCATCTTAAG	297
Qy	234	PheIlePheGlyPhePheIleSerIleAlaLeuLeuTyrTyrTyrSerSerLeuGlyTyr	253
Db	296	TTCAATTTCTGGTTTTCTGCTGCTGCGAGGATGATGATTTCTACTTCTCAAGCCGTGTTAC	237
Qy	254	LeuHisMetAsnTyrGlnThrThrIleuGlnArgValAlaMetValSerMetValAlaTyr	273
Db	236	ATTCAATGTTATCTGGAGGAGGCACTCGGTAAAGCTGGCCCTTGTTCACTGCAGGACAAAC	177
Qy	274	ValValGlnSerLeuProIleThrAspGlnLeuAspAspAsnIleSerValProLeuAla	293
Db	176	GTAGGAGAGTGCATTTCTGTGACTGAAGATGTATGATGACAAATATATCTGTTCTTTGGCC	117
Qy	294	ThrIleLeuAlaAlaTyrLeuSerPhe	302
Db	116	ACCATGCTGGTAGCTTTTCTCTGTTT	90

RESULT	8
LOCUS	CB261834
DEFINITION	CB261834 507 bp mRNA linear EST 06-NOV-2007 85-E8864-008-010-J22-pB12 MPIC-ADIS-008 Arabidopsis thaliana cDNA clone MPIDP76J2210Q 5-PRIME, mRNA sequence.
ACCESSION	CB261834
VERSION	CB261834.1 GI:32886607
KEYWORDS	EST.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicotyledons; rosids; eurooids II; Brassicales; Brassicaceae; Arabidopsi. 1 (bases 1 to 507) Schmid,K.J., Soehrensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
AUTHORS	

TITLE

JOURNAL single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
PUBMED Genome Res. 13 (6), 1250-1257 (2003)
12799357
Contact: Weisshaar B

FEATURES

Source

```

/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="C24"
/db_xref="GABI:601198"
/db_xref="taxon:3702"
/c1one="MP12p67J2210Q"
/r1ssue_type="seedling"
/dev stage="few days old seedlings"
/lab host="E. coli XL1-Blue MRF"
/c1one_l1b="MP12-AD15-008"
/note="Vector: pBluescript SK (-); Site 1: EcoRI, Site 2:
XhoI; cDNA library from Arabidopsis thaliana, accession
C24; seedling; Lambda ZAPII phage library was made at the
Max-Planck-Institute of Molecular plant Physiology, Goltm,
Germany and mass-excised at the Max-Planck-Institute for
Plant Breeding Research, Cologne, Germany; cloning sites
EcoRI-XhoI; Note: sequencing granted in the context of the
GABI Arabidopsis Verbund I; Genetic Diversity,
Establishment of high-efficiency SNP-based mapping tools
and development of methods for genome-wide mutation
detection; PI: Bernd Weisshaar Sequence submission managed
by RZPD/GABI-Primary database: http://gabi.rzpd.de This
clone is available from RZPD; contact RZPD (clone@rzpd.de)
for further information."
```

ORIGIN

Alignment Scores:	
Pred. No.:	1,53e-74
Score:	745.00
Percent Similarity:	100.00
Best Local Similarity:	100.0%
Query Match:	48.5%
DB:	6
Length:	507
Matches:	145
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-634-548-2 (1-304) X CB261834 (1-507)

[illegible]

REFERENCE 1 (bases 1 to 654)
 AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and
 TITLE An EST database from Sorghum: ovaries of varying immature stages
 JOURNAL Unpublished (2000)
 COMMENT Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Km. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Seq primer: PolyTMix
 High quality sequence start: 8
 High quality sequence stop: 628
 POLYA=No.

FEATURES
 source location/Qualifiers
 1..654
 /organism="Sorghum bicolor"
 /db_type="mRNA"
 /db_xref="taxon:4558"
 /clone_idb="Ovary 2 (OV2)"
 /note="Organ: Mix of ovaries of varying immature stages
 from 8-week-old plants; Vector: pBluescript II from lambda
 Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made
 from poly-A RNA in the cloning vector lambda Zap II.
 Clones to be sequenced were prepared by mass excision."

ORIGIN

Alignment Scores:
 Pred. No.: 4,74e-71 Length: 654
 Score: 716.00 Matches: 127
 Percent Similarity: 84.6% Conservative: 49
 Best Local Similarity: 61.1% Mismatches: 32
 Query Match: 46.6% Indels: 0
 DB: 2 Gaps: 0

US-10-634-548-2 (1-304) x BG412580 (1-654)

QY 88 PheGUSerLeuThrLysArgAsnValIleGlnGlnSerLeuSerArgLysLeuValHis 107
 Db 4 TTTCAGACGATCCACGACGCGGCTCATCGAAAAGATTGAGCAGAGAGGTTGTGCAC 63
 QY 108 IleLeuSerGlyLeuLeuPheValLeuAlaTrpProIlePheSerGlySerThrGluAla 127
 Db 64 GTGCTATCCGGCGCTCTGTCATGTCATCGCGCGCTTCACGCAATTGACAGAGACA 123
 QY 128 ArgTyrPheAlaAlaPheValProLeuValAsnGlyLeuArgLysLeuValIleAsnGlyLeu 147
 Db 124 CGGATTTTCGCTGACGTTTCCACTCTTGAATCCATAGAGCTTCTGATATATGCACTC 183
 QY 148 SerLeuSerProAsnSerMetLeuIleLysSerValThrArgGluGlyArgAlaGlu 167
 Db 184 CGTCTCTACACTGAGTGAAGCTCTAGTAAATCATGACGACGTAAGAGAAACCAAGAGAA 243
 QY 168 LeuLeuValGlyProLeuPheTyrValLeuAlaLeuLeuPheSerAlaValAlaPhePheTrp 187
 Db 244 TTGCTGAGAGGTCACAGTATATATGTTGTGCTGTTGTCAGTGTATTGATGCTTCGG 303
 QY 188 ArgGluSerProIleGlyMetIleSerLeuAlaMetMetCysGlyGlyAspGlyIleAla 207
 Db 304 CGGAGATCCCTGTTGGATGTCCTTTTTCATGATGATGATGATGATGATGATGATGATGAT 363
 QY 208 AspIleMetGlyArgLysPheGlySerThrLysIleProTyrAsnProArgLysSerTrp 227
 Db 364 GACATGTTGGAGAGAGGATATGCTCAGTGAAGCTGCATTCATTAAGAGAGAGCTGG 423
 QY 228 AlaGlySerIleSerMetPheIlePheGlyIlePheIleSerIleAlaLeuLeuTyrTyr 247
 Db 424 GCCCGAGACATCTCATGTCATTTCTGTTTCTGCTGCCGATGATATATGTTTAC 483
 QY 248 TyrSerSerLeuGlyTyrLeuHisMetAsnTrpGluThrThrLeuGlnArgValAlaMet 267

Db 484 TTTCAGACGCTTGATCATTTGATGATTTTGGACAGAGCAGCTTGTAAGCTGCGCTT 543
 QY 268 ValSerMetValAlaThrValValGluSerLeuProIleThrAspGluLeuAspAspAsn 287
 Db 544 GTTGCACTGAGCAGACACCGTAGTATCTCTGATGATGATGATGATGATGATGATGATGAT 603
 QY 288 IleSerValProLeuAlaThrIle 295
 Db 604 ATATCTGTCCTTGGCCACCATG 627

RESULT 11
 DN229569
 LOCUS DN229569/c 675 bp mRNA linear EST 01-MAR-2005
 DEFINITION MEST1065_F09.T7-1 UGA-zmsam-x22 Zea mays cDNA, mRNA sequence.
 ACCESSION DN229569
 VERSION DN229569.1 GI:60396702
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 675)
 Chen,H.D., Zhang,X., Zhou,R.L., Arias,L.A.C., Shendeiman,J.M.,
 Zazubovics,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J.
 and Schnable,P.S.
 Expressed Sequence Tags from B73 Maize Shoot Apical Meristems
 Unpublished (2004)
 CONTACT Patrick S. Schnable
 Schnable Laboratory
 Iowa State University
 205B R.U. Carver Co-Lab, Ames, IA 50011-3650, USA
 Tel: 515-294-0975
 Fax: 515-294-5256
 Email: schnable@iastate.edu.

FEATURES
 source location/Qualifiers
 1..675
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="Indred B73"
 /db_xref="taxon:4577"
 /tissue_type="Vegetative Shoot Apical Meristem (SAM) and
 leaf primordia staged p1-p4"
 /lab_host="X1L-Blue"
 /clone_idb="UGA-zmsam-x22"
 /note="Organ: Shoot apex; Vector: Uni-Zap XR; Site 1:
 EcoRI; Site 2: XhoI; This library was constructed by
 Xiaoan Zhang. Vegetative Shoot Apical Meristem (SAM) and
 leaf primordia staged p1-p4 from 14-17 day-after
 germination seedlings were quickly dissected into dry ice
 under a light microscope. Total RNA was isolated using
 Trizol and mRNA was purified with Dynal Oligo-dT25.
 ds-cDNA molecules were generated as follows. First-strand
 cDNA was prepared from oligo-dT selected mRNA by priming
 with an xhoI oligo-dT primer
 (5'-GACAGCAGACGAGACGAGACTGCTCGAGTTTCTTTTCTTTT).
 The resulting DNA:RNA hybrid was treated with RNase H and
 used as a template for DNA PolI-catalyzed second strand
 synthesis. After the addition of EcoRI adaptor, the
 ds-cDNAs were digested with XhoI and size-selected to be
 into the EcoRI and XhoI sites of the Uni-Zap XR vector.
 The lambda library was packaged with Gigapack III Gold
 packaging extract and was mass excised by X1L-Blue cells
 and ExSist helper phage. Excised phagmids were titrated
 in SOUR cells and plated onto LB-ampicillin agar plates.
 Base calling was conducted using Phred. Trimming was
 performed using Lucy with the following criteria:
 (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low
 complexity filter was applied and additional trimming was
 conducted to remove E. coli, vector, and organelle
 contamination. After processing ~30% of the sequences
 contained a minimum of 10 Ts at the beginning of the

sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."

ORIGIN

Alignment Scores:

Pred. No.: 2,66-69 Length: 675
Score: 701.00 Matches: 127
Percent Similarity: 83.4% Conservative: 44
Best Local Similarity: 62.0% Mismatches: 34
Query Match: 45.6% Indels: 0
Gaps: 0

US-10-634-548-2 (1-304) x DN229569 (1-675)

```

Qy 98 GlnGlnSerLeuSerArgLeuValHisIleLeuSerGlyLeuLeuPheValLeuAla 117
Db 673 GAAAGAGCTTGAAGAGAGGTTGTGACGCTATCCGCGTCTTCTTCATGTCATCT 614
Qy 118 TrpProIlePheSerGlySerThrGluAlaArgTyrPheAlaPheValProLeuVal 137
Db 613 TGGCCCCGTTCAGCAATTCACAGACACGATTTTCGCCGCCGTTGCCCTTCCTG 554
Qy 138 AsnGlyLeuArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMetLeuIleLys 157
Db 553 AACTCCATGAGGCTTCTGATATATGAGACTCCGCTCTACATGATGAGAGCTCTGTA 494
Qy 158 SerValThrArgGluGlyArgAlaGluGluLeuLeuLysGlyProLeuPheTyrValLeu 177
Db 493 TCAGTGACACGCGAAGAAACCAAGAGAAATTCGAGAGAGGTCCTATTAATGTCCTG 434
Qy 178 AlaLeuLeuPheSerAlaValPhePheTyrPargIleSerProIleGlyMetIleSerLeu 197
Db 433 GTGCTGCTGTTCAAGCTTTTACTTCTTGGCGCTGAGTCCCATCGGATGCTCTCTG 374
Qy 198 AlaMetMetCysGlyGlyAspGlyIleAlaAspIleMetGlyArgLysPheGlySerThr 217
Db 373 TCGAGTAGAGAGCGGCGGAGATGTTTGTCTGACATTTGTTGGAGAGATAGCTCAGCG 314
Qy 218 LysIleProTyrAsnProArgLysSerTrrAlaGlySerIleSerMetPheIlePheGly 237
Db 313 AAGCTGCATTCATCAATCGAAGAGAGCTGGCGCGGAGAGATCTCGATGTTCAATTCCTG 254
Qy 238 PhePheIleSerIleAlaLeuLeuTyrTyrTyrSerSerLeuGlyTyrLeuHisMetAsn 257
Db 253 TTCCTGCTGCTCGCATGATGATGCTTACTTCTCAAGCTCGGTTACTATGATGATC 194
Qy 258 TrpGluThrThrLeuGlnArgValAlaMetValSerMetValAlaThrValAlaGluSer 277
Db 193 TGGGAAGAGGACCTTGTAAGCTGGCGCTGTGTGACATGACGACAGTAGTAGAGTGC 134
Qy 278 LeuProIleThrAspGlnLeuAspAspAsnIleSerValProLeuAlaThrIleLeuAla 297
Db 133 GTTCTGTGACCGAAGTTGTAGATGACAAATATCTGTTCTTGGCCACCATGCTGTA 74
Qy 298 AlaTyrLeuSerPhe 302
Db 73 GCTTTCCTCTTCTT 59

```

RESULT 12
CK297713 941 bp mRNA linear EST 02-AUG-2004
LOCUS CK297713
DEFINITION EST060427 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMDA80 5'
end, mRNA sequence.

ACCESSION CK297713.1 GI:39884376
VERSION CK297713
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiales, Solanales, Solanaceae, Nicotiana.

REFERENCE

AUTHORS

1 (bases 1 to 941)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Skaskiewicz, B., Jin, H. and Baker, B.

TITLE

Generation of EST sequences from Nicotiana benthamiana

JOURNAL

Unpublished (2003)

Other ESTs: EST760428

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics

Institute via <http://genome.arizona.edu/orders/>.

Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source

1..941

/organism="Nicotiana benthamiana"

/mol_type="mRNA"

/db_xref="taxon:4100"

/clone="NBMDA80"

/cissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"

/lab_host="DH10B-TonA"

/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI, Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C, 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Pseudomonas syringae pv campestris 12 hr, 18hr;
Xanthomonas campestris pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Alignment Scores:

Pred. No.: 1,876-66 Length: 941
Score: 678.00 Matches: 148
Percent Similarity: 65.6% Conservative: 39
Best Local Similarity: 51.9% Mismatches: 49
Query Match: 44.1% Indels: 49
Gaps: 6
DB: 7

US-10-634-548-2 (1-304) x CK297713 (1-941)

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Qy 16 ArgPheGlyAsn-----AsnSerLeuThrThrHis----- 25
Db 120 CGTTCTCGAATCTGCGCTTCTCTCTCACTGATCAACCCACACTTACATTGGCGGA 179
Qy 26 ArgPheCysSerPro-----GlyPheLeuIleSerSerProCysPheIleGlyLeuThr 43
Db 180 CGATTCTTCTGCGGTCACAGATCCGACCGCGTCTGATCTGCGGACCGCGGTTTACA 239
Qy 44 GlyMetGlySerAlaThrGlnLeuArgAlaArgArgSerLeuIleSerSerAlaValAla 63
Db 240 GGTGCTTTGATGCT-----ATAATTGAGATGCG----- 269
Qy 64 ThrAsnSerLeuLeuHisAspValGlyAlaThrValAlaValLeuGlyGlyAlaTyrAla 83
Db 270 ---GGCTAGAGCTGACAGATGCGGAGCCACCGGCTTGGTCATGCTGGTCTTACGCG 326
Qy 84 LeuValLeuSerPheGlySerLeuThrLysArgAsnValIleGlnGlnSerLeuSerArg 103
Db 327 CTGTTCCACTTTCGATTTCTTATCCAGGACCAAGCTCATTAAGACAAATTTAAGCACA 386
Qy 104 LysLeuValHisIleLeuSerGlyLeuLeuPheValLeuAlaTrrProIlePhe----- 121
Db 387 AAGCTTTCACATATTTCTGCTGCTTTTAAAGGCTTCTGCGCAATTTTCAAGTAT 446
Qy 121 ----- 121

```

Db 447 TATTTGCTTACATATATGATGCAAAACCATATTGGAAGTTCTCACTGATGATTTAG 506
 Qy 122 -----SerGlySerThrGluAlaArgTyrPheAlaAlaPheValProLeuValAs 138
 Db 507 ATGTTAGATTGATGATCAAGATGAGGACGCTACTTCTCTGATGTTCCGCTACAAA 566
 Qy 138 nGlyLeuArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMetLeuIleLeuSe 158
 Db 567 CTGTTTGAGACTTGATGATTTATGAGCCCTTCTTGCTACTGATGAGGACCTTCAAAATC 626
 Qy 158 TValThrArgGluGlyArgAlaGluGluLeuLeuValGlyProLeuPheTyrValLeuAl 178
 Db 627 TGTACTCGGAGAGAAAGCAGAAAGATGCTTAGAGGGCCTCATATATATGTTCTAGT 686
 Qy 178 AlLeuLeuPheSerAlaValPhePheTyrArgGluSerProIleGlyMetIleSerLeuAl 198
 Db 687 GTTATATTTGACCGCACTTCTCTTTTGCGTGAAGCACACAGTGAAGTAATTTCTTAGC 746
 Qy 198 AMetMetCysGlyGlyArgGlyIleAlaAspIleMetGlyArgLysPheGlySerThrLy 218
 Db 747 AATGATGTGTGCTGATGATGATGATGCTGATATTTCTGAGAGAGGTTGGGTCATMAA 806
 Qy 218 sIleProTyrAsnProArgLysSerTyrAlaGlySerIleSerMetPheIlePheGlyPh 238
 Db 807 AATCCCTATATATAACAGAAAGTTGGCTGCTAGCCCTCCACAGTTTGTCTCGGTTT 866
 Qy 238 ePheIleSerIleAlaLeuLeuTyrTyrTyrSerSerLeuGlyTyrLeuIleMetAsnTr 258
 Db 867 CTGGTGTGCATGTTGGATGCTCTATTAATCTTCCTGCTGAGATATCTTCACTGAGATTG 926
 Qy 258 pGluThrThrLeu 262
 Db 927 GGTTCACACTGTA 939
 RESULT 13
 LOCUS A1712188 623 bp mRNA linear EST 02-PEB-2000
 DEFINITION 60506SD08.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
 ACCESSION A1712188
 VERSION A1712188.1 GI:5006126
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 623)
 AUTHORS Walbot, V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 605065 row: D column: 08.
 FEATURES
 SOURCE
 1. 623
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultiivar="Oh1043"
 /db_xref="taxon:4577"
 /tissue_type="nucellar, embryo, and endosperm"
 /dev_stage="10-14 days post-pollination"
 /lab_host="DHS(alpha)"
 /clone_lib="605 - Endosperm cDNA library from Schmidt lab"
 /note="Organ: Kernel; Vector: PAD-GAL4-2'; Site: 1: EcoRI;
 Site 2: XhoI; Kernel endosperm cDNA library from Schmidt
 lab"

ORIGIN
 Alignment Scores:
 Pred. No.: 6,28e-66 Length: 623
 Score: 671.00 Matches: 121
 Percent Similarity: 82.7% Conservative: 41
 Best Local Similarity: 61.7% Mismatches: 34
 Query Match: 43.7% Indels: 0
 DB: 1 Gaps: 0
 US-10-634-548-2 (1-304) x A1712188 (1-623)
 Qy 107 HisIleLeuSerGlyLeuLeuPheValLeuAlaTrpProIlePheSerGlySerThrGly 126
 Db 621 CACGTGCTATCCGGCGCTGCTTTCATGTCATCTTGCCCTTTCAGCATATTCACAGAA 562
 Qy 127 AlaArgTyrPheAlaAlaPheValProLeuValAsnGlyLeuArgLeuValIleAsnGly 146
 Db 561 GCCCGATATTGCGCGGGTGTCCCGTTCCTGAATCCATGAGGCTTCTGATATATGGA 502
 Qy 147 LeuSerIleSerProAsnSerMetLeuIleLysSerValThrArgGluGlyArgAlaGlu 166
 Db 501 CTCGCTCTACACTGATGAGACTGTGTAAATCAGTGACACGTGAAGAAACCAAGAG 442
 Qy 167 GluLeuLeuValGlyProLeuPheTyrValLeuAlaLeuLeuPheSerAlaValPhePhe 186
 Db 441 GAATTCCTGAGAGATCCACTTATTAATGCTGCTGCTGCTGCTTTCAGCGCTTTAGTCTTC 382
 Qy 187 TTrpArgGluSerProIleGlyMetIleSerLeuAlaMetMetCysGlyGlyAspGlyIle 206
 Db 381 TGGCGTAGTCCCGCATCGGATCGTCTCTGTCGATGATGACGGGCGGATGTTT 322
 Qy 207 AlaAspIleMetGlyArgLysPheGlySerThrLysIleProTyrAsnProArgLysSer 226
 Db 321 GCTACATTCGCGAGAGAGGTATGCTCACGAGGATCCATTCATTCGGAAGAGGC 262
 Qy 227 TrpAlaGlySerIleSerMetPheIlePhePheIleSerIleAlaLeuLeuTyr 246
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 Qy 267 MetValSerMetValAlaThrValValGluSerLeuProIleThrAspGlnLeuAspAsp 286
 Db 141 CTGTGTGACATGACAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 82
 Qy 287 AsnIleSerValProLeuAlaThrIleLeuAlaAlaTyrLeuSerPhe 302
 Db 81 AACATATCTGTTCTTTGGCCACCATGCTGTAGCTTTTCTTGTGTT 34
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 5', mRNA sequence.
 ACCESSION CA277256
 VERSION CA277256.1 GI:35998743
 KEYWORDS EST.
 SOURCE Saccharum officinarum
 ORGANISM Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Saccharum; Saccharum officinarum
 complex.
 REFERENCE 1 (bases 1 to 690)
 AUTHORS Vertore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
 TITLE The libraries that made SUGEST
 JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 COMMENT Centro de Biologia Molecular e Engenharia Genetica
 Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089
 Email: parruda@unicamp.br
 Clone distribution: clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at
 http://www.bcccenter.fcav.unesp.br
 Plate: 014 row: H column: 08
 Seq primer: 17 Promoter Primer.
 Location/Qualifiers

FEATURES

source

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 /clone_lib="SD2"
 /note="Organ: Developing seeds (small insert library);
 Vector: pSport1; Site 1: SalI; Site 2: NotI; An
 unidirectional cDNA library generated from [Developing
 seeds (small insert library)]. cDNA was prepared from
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 (Invitrogen). The double-strand cDNAs were fractionated
 in a sepharose CL-2B 40cm-columns and fragments sizing
 between 0.8 and 1.5 Kb were directionally cloned into the
 vector. Details of each source of RNA and library
 construction can be obtained at
 http://succeet.lad.ic.unicamp.br/public"

ORIGIN

Alignment Scores:

Pred. No.: 3,586-65 Length: 690
 Score: 665.00 Matches: 120
 Percent Similarity: 81.0% Conservative: 42
 Best Local Similarity: 60.0% Mismatches: 38
 Query Match: 43.3% Indels: 0
 DB: 6 Gaps: 0

US-10-634-548-2 (1-304) x CA277256 (1-690)

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 629 ATTCCAGAAAGAACGCGATTTCGCGCAGTTGTTCTTGACTTCCATCCATTAAGGCTT 570
 143 ValIleAsnGlyLeuSerIleSerProAsnSerMetLeuIleLeuSerValThrArgGlu 162
 569 CTGACATACGAGACTCCGCTCTACACTGATGAAGCTCTAGTAAATCAGTGACAGTGAA 510
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 183 AlaValPhePheThrArgGluSerProIleGlyMetIleSerLeuAlaMetMetCysGly 202
 449 GTTTTAGTCTCTGGGAGAGTCCCATTTGGATTTGATCCTTGTGATGATGAGTGT 390
 203 GlyAspGlyIleAlaAspIleMetGlyArgGlyPheGlySerThrLeuIleProTyrAsn 222
 389 GGGGATGGTTTGTCTGACATTTGTTGGGAGAGATGAGTCTGAGTGAAGTGCATTCAT 330
 223 ProArgGlySerTTPAlaGlySerIleSerMetPheIlePheGlyPhePheIleSerIle 242
 329 GAGAGAAAGATTGGGCGGAGAGCATCTCATGTTCAATTTCTGTTTCTGCTGCTGCG 270
 243 AlaLeuLeuTyrTyrSerSerLeuGlyTyrLeuHisMetAsnTTPGlnThrHisLeu 262
 269 ATGATGATTTCTACTTCAGAGCCCTGGGTTTCAATTCATTCATTCGAGGAGAGGACATC 210
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RESULT 15
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 ACCESSION AY109900
 VERSION AY109900.1 GI:21213810
 KEYWORDS
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 650)
 Gardner,J., Schroeder,S., Polacco,M.L., Sanchez-Villeda,H.,
 Fang Z., Morgante,M., Landewe,T., Fengler,K., Useche,F.,
 Hanafey,M., Tingey,S., Chou,H., Wing,R., Soderlund,C. and Coe,E.H.
 Jr.

REFERENCE

AUTHORS

TITLE

Anchoring 9,371 maize expressed sequence tagged unigenes to the
 bacterial artificial chromosome contig map by two-dimensional
 overgo hybridization
 Plant Physiol. 134 (4), 1317-1326 (2004)

JOURNAL

PUBMED

2 (bases 1 to 650)

AUTHORS

Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitelst,M.S.,
 Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.

TITLE

Maize Mapping Project/Dupont Consensus Sequences for Design of

JOURNAL

Overgo Probes

REFERENCE

Unpublished (2002)

AUTHORS

3 (bases 1 to 650)
 Coe,E.H.

JOURNAL

Direct Submission

COMMENT

Submitted (25-APR-2002) Maize Mapping Project, University of

JOURNAL

Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones,
 these are publicly available from ZmDB and may be found by BLAST
 searching at MST, maizeMap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Malbot, Stanford or Pat
 Schnable, Iowa State, then clones may be requested from ZmDB:
 www.zmdb.iastate.edu.

FEATURES

Location/Qualifiers

1. 650
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 /clone_lib="Maize Mapping Project/Dupont Consensus
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 /note="this sequence is part of a project of EST
 assemblies resulting from the application of public
 contigs to seed Dupont contigs; this resource was
 assembled by Dupont as part of a collaboration for the
 overgo addressing of BACs in conjunction with the Maize
 Mapping Project"

ORIGIN

Alignment Scores:

Pred. No.: 2,076-64 Length: 650
 Score: 658.00 Matches: 119
 Percent Similarity: 81.6% Conservative: 41
 Best Local Similarity: 60.7% Mismatches: 36
 Query Match: 42.8% Indels: 0
 DB: 4 Gaps: 0

US-10-634-548-2 (1-304) x AY109900 (1-650)

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 16, 2006, 22:17:48 ; Search time 217 Seconds
(without alignments)
2490.225 Million cell updates/sec

Title: US-10-634-548-2

Perfect score: 1536
Sequence: 1 MAATLPLSPIHQLCRFGNN.....DDNISVPLATILAVLSRGY 304

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118.5	7.7	1664976	3 US-08-916-421B-1	Sequence 1, Appli
2	118.5	7.7	1664976	3 US-09-692-570-1	Sequence 1, Appli
3	105.5	6.9	1495	3 US-09-248-796A-2050	Sequence 201, Ap
4	105.5	6.9	1726	3 US-09-605-703B-491	Sequence 489, App
5	105.5	6.9	2187	4 US-09-605-703B-489	Sequence 489, App
6	100.5	6.5	858	3 US-09-328-352-3131	Sequence 311, Ap
7	100.5	6.5	891	3 US-09-540-236-198	Sequence 198, App
8	100.5	6.5	99629	3 US-09-596-002-37	Sequence 37, Appl
9	99	6.4	870	3 US-09-489-039A-5219	Sequence 5219, Ap

10	99	6.4	1548	3 US-09-328-352-964	Sequence 964, App
11	98.5	6.4	1152	3 US-09-710-279-2167	Sequence 2167, Ap
12	98.5	6.4	1359	3 US-09-134-001C-1098	Sequence 1098, Ap
13	98.5	6.4	3108	3 US-09-710-279-3427	Sequence 3427, Ap
14	97.5	6.3	903	3 US-09-543-681A-282	Sequence 282, App
15	97	6.3	1227	3 US-09-543-681A-650	Sequence 650, App
16	97	6.3	1296	3 US-09-549-848B-5	Sequence 5, Appli
17	97	6.3	1266	3 US-09-688-069-5	Sequence 3049, Ap
18	97	6.3	1341	3 US-09-134-000C-3049	Sequence 8008, Ap
19	97	6.3	1383	3 US-09-902-540-8008	Sequence 814, App
20	97	6.3	7021	3 US-09-902-540-8008	Sequence 3797, Ap
21	96	6.2	993	3 US-09-489-039A-3797	Sequence 1, Appli
22	95.5	6.2	1830121	3 US-09-557-884-1	Sequence 1, Appli
23	95.5	6.2	1830121	3 US-09-643-990A-1	Sequence 1, Appli
24	95.5	6.2	1830121	3 US-10-158-865-1	Sequence 3968, Ap
25	95	6.2	288	3 US-09-315-284A-3968	Sequence 18, Appl
26	95	6.2	1442	2 US-08-468-763-18	Sequence 18, Appl
27	95	6.2	1442	2 US-08-393-996A-18	Sequence 1, Appli
28	95	6.2	2051	2 US-08-672-814D-1	Sequence 1, Appli
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30	95	6.2	2051	3 US-09-282-218A-1	Sequence 1, Appli
31	95	6.2	2103	3 US-09-282-218A-13	Sequence 13, Appl
32	94.5	6.2	1275	3 US-09-134-001C-2172	Sequence 73, Appl
33	94.5	6.2	1335	3 US-09-540-236-73	Sequence 4013, Ap
34	94.5	6.2	3840	3 US-09-710-279-4013	Sequence 4013, Ap
35	94.5	6.2	4235	3 US-09-710-279-4041	Sequence 34, Appl
36	94.5	6.2	89047	3 US-09-596-002-34	Sequence 919, App
37	94	6.1	756	3 US-09-134-000C-919	Sequence 568, App
38	94	6.1	1689	3 US-09-328-352-568	Sequence 203, App
39	94	6.1	3230	3 US-08-961-527-203	Sequence 414, App
40	93.5	6.1	630	3 US-09-583-110-414	Sequence 1052, Ap
41	93.5	6.1	682	3 US-09-107-433-1052	Sequence 2001, Ap
42	93.5	6.1	1230	3 US-09-710-279-2001	Sequence 2305, Ap
43	93.5	6.1	1230	3 US-09-710-279-2305	Sequence 3698, Ap
44	93.5	6.1	1245	3 US-09-489-039A-3698	Sequence 2966, Ap
45	93	6.1	927	3 US-09-328-352-2966	

ALIGNMENTS

RESULT 1
US-08-916-421B-1
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Built et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus jannaschii
Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature

Alignment Scores: 15.1 length: 1664976
Pred. No.: 118.50 Matches: 51
Score: 42.08 Conserved: 43
Percent Similarity: 22.84 Mismatches: 59
Best Local Similarity: 7.7% Indels: 71
Query Match: 3 Gaps: 13
DB: 3

US-10-634-548-2 (1-304) x US-08-916-421B-1 (1-1664976)

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Qy 112 LeuSerPheValLeuAlaTrpProIlePheSerGlySerThr 125
Db 393796 GTTATTAATGACATTTTCAGTTTAAATTAATAAACAATTAATTCATTAAATGTT 393855
Qy 126 -----GluAlaArgTyrPheAlaIle-----PheValProLeuVal 137
Db 393856 AGTATGATTATGATCTGCTATATTTTATGTAAGATATTAATTCATCAATAGTA 393915
Qy 138 AaGlyLeuAaGlyLeuValIleAaGlyLeuSerIleSerProAaSerMetLeuIleLys 157
Db 393916 TCAGATTAA-----TTAAAT-----CTCTGTAAA 393939
Qy 158 SerValThrAaGlyGlyAaGlyAaGlyLeuLeuLeuLeuLeuLeuLeuLeu 177
Db 393940 AGAGAAAAAGAGATGA-----AAAGAGCATATTAATTCCTATTT 393981
Qy 178 AlaLeuLeuPheSer-----AlaValPhePheTrpArgGlu 189
Db 393982 GGTATGTTAACTCTCTTAATTTTAAATGATGATTAATAAGCTGATTTT----- 394032
Qy 190 SerProIleGlyMetIleSerLeuAlaMetMetCysGlyGlyAaGlyIleAlaAaPhe 209
Db 394033 -----GGCATCTTGATTTGCTCTGT-----GGGATTCCTTATGCTACTATA 394074
Qy 210 MetGlyAaGlyPheGlySerThrIleProIleProIleProIleProIleProIle 229
Db 394075 ATAGGCATTAG-----GGAATAATTAATAATAATAC-----TTTGAAAA 394116
Qy 230 SerIleSerMetPheIlePheGlyPhePheIleSerIleAlaLeuLeuTyr----- 247
Db 394117 ACGGTGAGGATTTTA-----GCATTTTATCTGCTCTATTAATTTATTCATTT 394173
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Qy 288 IleSerValPro 291
Db 394255 CTCTATCTTCT 394266

RESULT 2
US-09-692-570-1
Sequence 1, Application US/09692570
Patent No. 6797466
GENERAL INFORMATION:
APPLICANT: Built et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
Patent No. 6797466
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275C1
CURRENT APPLICATION NUMBER: US/09/692,570
PRIOR FILING DATE: 2003-01-14
CURRENT APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
PRIOR APPLICATION NUMBER: US 08/916,421

PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (146948)..(146948)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature

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OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g

Alignment Scores:
Pred. No.: 15.1 Length: 1664976
Score: 118.50 Matches: 51
Percent Similarity: 42.0% Conservative: 43
Best Local Similarity: 22.8% Mismatches: 59
Query Match: 7.7% Indels: 71
Gaps: 13
DB: 3

US-10-634-548-2 (1-304) x US-09-692-570-1 (1-1664976)
Qy 92 ThrlyArGaenValllgInGInSerIeuSerArGlyLeuValHlslleuSerGly 111
Db 393736 ACTAAAAAGCTTGAACCTTTGAGAGAGATTATACACAAACATCATTTAGTTTGGA 393795
Qy 112 LeuIeuPheValIeuAlaTrpProIlePheSerGlySerThr----- 125
Db 393796 GTTTATATGACATTTCAGCTTTTAAATTTAAAAAACATTAATATCCATTAAATGTT 393855
Qy 126 -----GluAlaArgTyPheAlaIa-----PheValProIeuVal 137
Db 393856 AGTATAGTATTGGATCGCTGCTTATTTTATATGTAAGATATATACCAATAGTA 393915
Qy 138 AsnGlyLeuAlaGlyLeuValIleAsnGlyLeuSerIleSerProAsnSerMetLeuIleVal 157
Db 393916 TCAGATTTA-----TTAAAT-----CTCTGTAAA 393939
Qy 158 SerValThrArgGluGlyArgAlaGluGluLeuLeuValGlyProIeuPheTyPheValLeu 177
Db 393940 AGAGAAAAAGAGACAGCA-----AAAGAGGACGATATATCTTGGCAT 393988
Qy 178 AlaIeuIeuPheSer-----AlaValPhePheTrpArgGlu 189

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Db 393982 GGTATGTTATCTCATTTATTTATGATGATATAAAGCTGATTTTTT----- 394032
Qy 190 SerProilegylMetIleSerleuAlaMetMetCysgylgylAspGlyIleAlaAspIle 209
Db 394033 -----GGCATCTGCTGATTTATCTCTGTT-----GGGCAATCTTACTTACTATTA 394074
Qy 210 MetGlyArglyPheGlySerThrIlyValIleProGlyPheProArglySerThrIlyVal 229
Db 394075 ATAGGCAATTAGA---GAAAAATTAAAAAATAATAC-----TTTGAAAA 394116
Qy 230 SerIleSerMetPheIlePheGlyPhePheIleSerIleAlaIleLeuIleTyr----- 247
Db 394117 ACGGTGAGGATTTTAA---GCATTTTATCTCTGCTCATTTATTTATATCCATTT 394173
Qy 248 TyrSerSerLeuGlyTyrLeuHISMetCAsnTrpGluThrThrLeuGlnArgValAlaMet 267
Db 394174 TATGGAACCTTATGGG-----ATTTTC 394194
Qy 268 ValSerMetValAlaIleThrValValGluSerLeuProIleThrAspGlnLeuAspAsn 287
Db 394195 GTAGCTTTAATCTCAGCATTTATTTGAAATTTGTAAGTAAGAAAAATAAGAAATGATGACAAAT 394254
Qy 288 IleSerValPro 291
Db 394255 CTCTATCTTCT 394266

RESULT 3
US-09-248-796A-2050
; Sequence 2050, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2050
; LENGTH: 495
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-2050

Alignment Scores:
Pred. No.: 0.00108 Length: 495
Score: 105.50 Matches: 38
Percent Similarity: 44.5% Conservative: 35
Best Local Similarity: 23.2% Mismatches: 66
Query Match: 6.9% Indels: 25
DB: 3 Gaps: 8

US-10-634-548-2 (1-304) x US-09-248-796A-2050 (1-495)
Qy 152 AenSerMetLeuIleLeuSerValThrArgGluGlyArgAlaGluGluLeuLeuLeuGly 171
Db 4 AATGTACCGTCATCTCATTTGTATTTAGACACAAACGAATCAATCA---TATACCGG 60
Qy 172 ProLeuPheTyrValLeuAlaLeuLeuPheSerAlaValIlePheThrIleArgGluSerPro 191
Db 61 ACACCTTTTATTTATTTGGTGGTGTGTTGATT-----GTGCTTATGCTTATTCACAAAGAC 114
Qy 192 IleGlyMetIleSerLeuAlaMetMetCysgylgylAspGlyIleAlaAspIleMetGly 211
Db 115 ATTCTGTGTTGAGCATTTTATTTATTTAGTTGGGACAGACACTGCACTTTCACCTTTGGT 174
Qy 212 ArgIlyPheGlySerThrIlyValIleProGlyPheProArg-----IlySerTrp 227

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Db 175 AGACATTCGGTAA-----TATATCCACAGATTGCCAGCGGTAAATCCCTTA 222
Qy 228 AlaGlySerIleSerMetPheIle-----PheGlyPhe 238
Db 223 GCAAGCTCTCTGCTGATGTTGTTAACCAGATTGTTAGTCCCTATTTGTTGATATGCTAT 282
Qy 229 PheIleSerIleAlaLeuLeuTyrTyrIleSerSerLeuGlyTyrLeuHISMetCAsnTrp 258
Db 223 TTC-----ATTCCTCAATATATACATTTGGAACCAACAGAGTAATATCTACGAAATGCC 336
Qy 259 GluThrThrLeuGlnArgValAlaMetValSerMetValAlaThrValValGluSerLeu 278
Db 337 TCATCAACAAGTTAGATTACCAATTTATCTTGTGATTGGGTGATTAACCTAGATT 396
Qy 279 ---ProIleThrAsp-----GlnLeuAspAsnIleSerValProLeuAlaThrIle 295
Db 397 TCTGAAGTAATGATTAGTGTGATTTGATGATTAATCCCAATCCAGTTTGGAGTGA 456
Qy 296 LeuAlaIleTyr 299
Db 457 AACTGTATTTAT 468

RESULT 4
US-09-605-703B-491
; Sequence 491, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroeger, Burkhard
; APPLICANT: Schroeder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,318
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 491
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (101)..(1726)
; OTHER INFORMATION: PRXA02898
US-09-605-703B-491

Alignment Scores:
Pred. No.: 0.0084 Length: 1726
Score: 105.50 Matches: 68
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.9% Mismatches: 93
Query Match: 6.9% Indels: 72
DB: 4 Gaps: 13

US-10-634-548-2 (1-304) x US-09-605-703B-491 (1-1726)
Qy 6 ProLeuSerPro-----IleAsnHISGlnLeuCyArgPheGlyAsnAsn 20
Db 499 CCGTGAACCCCTGGGTGGGCGGACAGACAGATCACTGCTCTGTGTGGTGAAGACAC 558
Qy 21 SerLeuThrThrIleArgPheCysSer-----ProGlyPheLeu----- 33
Db 559 CATGCTGGCTCTTCGGCTCTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 618
Qy 34 ---IleSerSerPro-CyPheIleGlyLeuThrGlyMetGlySerAlaThrGlnLeuArg 52
Db 619 CATTCAGCTGCTCATTAATCACTGGGATGCCG---ATGGGATCCAGCTT----- 667

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QY 52 gAlaArgSerLeuIleSerSerAlaValAlaThrAnSerLeuHisAspValG1 72
DB 668 -----GGCTTGAATCCTCTTCGACGTGTTACCGGCTCGATATG----- 706
QY 72 yAlaThrValAlaValLeuGlyGlyAlaTyrAla----- 83
DB 707 -GGCACCCTGTCACATTTGAGCGCGTGGCTCGCTCGTGCAGGTAGATTAA 765
QY 84 -----LeuValIleuSerPheGluSerLeuThrIleAspGlnValIleGlnGlnSe 100
DB 766 GCCTGTGAGAGCAATGCGCAATGAAACCACTATGCTTCATGATATGGCGGAC 825
QY 100 rLeuSerArgIleValAlaIleLeuSerGlyLeuPheValAlaTyrPro1 120
DB 826 GATCACCGGTGGCATCTTCTAGCACTC---GGCATCATCTTGGATTGCCGGCGCAT 882
QY 120 ePheSerGlySerThrGluAlaArg-----TyrPheAlaAlaPheVa 134
DB 883 GATGACTGATCTTCACCGCTACTGTTCCATCTGAGGCGCATTTGGTCTGTGT 942
QY 134 1-----ProLeuValAsnGlyLeuAr 141
DB 943 CATCGTGGGTACGTTCTCTTCTACACAGCGCTTCATGCTGTGGTGGTGGCTGG 1002
QY 141 gLeuValIleAsnGlyLeuSerIleSerProAnSerMetLeuIleYSerValThrAr 161
DB 1003 CAAGTTATCGGTGCACCGTTGGACGCTTGGAAAGCTTGTGCGACCACTCCAAAGC 1062
QY 161 gGluGlyArgAlaGluGluLeuLeuGlyPheLeuPheTyrValLeuAlaLeuLeuPh 181
DB 1063 AAACCTCGCGCTACCGCACTACAGCGTTCGCACTGACGTTGGCATTTGCTAGTG-- 1120
QY 181 eSerAlaValPhePheTyrArgGluSerProIleGlyMetIleSerLeuAlaMetMeCy 201
DB 1121 -----ACTGCAATTTGGCATGCTTTCTGCAACCATAGAG-- 1153
QY 201 sGlyGlyAspGlyIleAlaAspIleMetGlyArgIlePheGlySerThrIleProTy 221
DB 1154 -----GACGCAAGTCCGACATATGCGGAGACGATACCGACGATTAATCTGTGA 1206
QY 221 rAnPProArgIleSerTyrAlaGlySerIleSerMet 233
DB 1207 GGGACCAACCAAC-----GGTTCATCACCATG 1234

RESULT 5
US-09-605-703B-489
/ Sequence 489, Application US/09605703B
/ Patent No. 6962989
/ GENERAL INFORMATION:
/ APPLICANT: Pompeius, Markus
/ APPLICANT: Kroger, Burkhard
/ APPLICANT: Schroder, Hartwig
/ APPLICANT: Zelder, Oskar
/ APPLICANT: Haberer, Gregor
/ TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
/ FILE REFERENCE: BGI-123CP
/ CURRENT APPLICATION NUMBER: US/09/605,703B
/ PRIOR FILING DATE: 2000-06-27
/ PRIOR APPLICATION NUMBER: 60/142,764
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: 60/152,318
/ PRIOR FILING DATE: 1999-09-03
/ NUMBER OF SEQ ID NOS: 2934
/ SEQ ID NO 489
/ LENGTH: 2187
/ TYPE: DNA
/ ORGANISM: Corynebacterium glutamicum
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (101)..(2164)
/ OTHER INFORMATION: RXN01071

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US-09-605-703B-489
Alignment Scores:
Pred. No.: 0.0124 Length: 2187
Score: 105.50 Matches: 68
Percent Similarity: 39.6% Conservative: 40
Best Local Similarity: 24.9% Mismatches: 93
Query Match: 6.9% Indels: 72
DB: 4 Gaps: 13

US-10-634-548-2 (1-304) x US-09-605-703B-489 (1-2187)
QY 6 ProLeuSerPro-----IleAnHisGlnLeuCyValGlyPheGlyAsnAn 20
DB 499 CTGCGAGCCCTTGGGTGGCGGCGCCAGACAGATACCTGCTGTGTGTGGAGGAC 558
QY 21 SerLeuThrThrIleAspGlyPheCysSer-----ProGlyPheLeu----- 33
DB 559 CATCGTTGGCTCTTGGCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 618
QY 34 ---IleSerSerPro-CysPheIleGlyLeuThrGlyMetGlySerAlaThrGlnLeuAr 52
DB 619 CATTTACCTGTCTCTCAATACCTGGGATCGCG---ATGGATCCAGCGTT----- 667
QY 52 gAlaArgSerLeuIleSerSerAlaValAlaThrAnSerLeuHisAspValG1 72
DB 668 -----GGCTTGAATCCTCTTCGACGTGTTACCGGCTCGATATG----- 706
QY 72 yAlaThrValAlaValLeuGlyGlyAlaTyrAla----- 83
DB 707 -GGCACCCTGTCACATTTGAGCGCGTGGCTCGCTCGTGCAGGTAGATTAA 765
QY 84 -----LeuValIleuSerPheGluSerLeuThrIleAspGlnValIleGlnGlnSe 100
DB 766 GCCTGTGAGAGCAATGCGCAATGAAACCACTATGCTTCATGATATGGCGGAC 825
QY 100 rLeuSerArgIleValAlaIleLeuSerGlyLeuPheValAlaTyrPro1 120
DB 826 GATCACCGGTGGCATCTTCTAGCACTC---GGCATCATCTTGGATTGCCGGCGCAT 882
QY 120 ePheSerGlySerThrGluAlaArg-----TyrPheAlaAlaPheVa 134
DB 883 GATGACTGATCTTCACCGCTACTGTTCCATCTGAGGCGCATTTGGTCTGTGT 942
QY 134 1-----ProLeuValAsnGlyLeuAr 141
DB 943 CATCGTGGGTACGTTCTCTTCTACACAGCGCTTCATGCTGTGGTGGTGGCTGG 1002
QY 141 gLeuValIleAsnGlyLeuSerIleSerProAnSerMetLeuIleYSerValThrAr 161
DB 1003 CAAGTTATCGGTGCACCGTTGGACGCTTGGAAAGCTTGTGCGACCACTCCAAAGC 1062
QY 161 gGluGlyArgAlaGluGluLeuLeuGlyPheLeuPheTyrValLeuAlaLeuLeuPh 181
DB 1063 AAACCTCGCGCTACCGCACTACAGCGTTCGCACTGACGTTGGCATTTGCTAGTG-- 1120
QY 181 eSerAlaValPhePheTyrArgGluSerProIleGlyMetIleSerLeuAlaMetMeCy 201
DB 1121 -----ACTGCAATTTGGCATGCTTTCTGCAACCATAGAG-- 1153
QY 201 sGlyGlyAspGlyIleAlaAspIleMetGlyArgIlePheGlySerThrIleProTy 221
DB 1154 -----GACGCAAGTCCGACATATGCGGAGACGATACCGACGATTAATCTGTGA 1206
QY 221 rAnPProArgIleSerTyrAlaGlySerIleSerMet 233
DB 1207 GGGACCAACCAAC-----GGTTCATCACCATG 1234

RESULT 6
US-09-328-352-3131
/ Sequence 3131, Application US/09328352
/ Patent No. 6562958
/ GENERAL INFORMATION:

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? APPLICANT: Gary L. Breton et al.
? TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
? TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
? FILE REFERENCE: GTC99-03PA
? CURRENT APPLICATION NUMBER: US/09/328,352
? CURRENT FILING DATE: 1999-06-04
? NUMBER OF SEQ ID NOS: 8252
? SEQ ID NO 3131
? LENGTH: 858
? TYPE: DNA
? ORGANISM: Acinetobacter baumannii
US-09-328-352-3131

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Alignment Scores:		
Pred. No.:	0.0115	Length: 858
Score:	100.50	Matches: 48
Percent Similarity:	38.9%	Conservative: 40
Best local Similarity:	21.2%	Mismatches: 83
Query Match:	6.5%	Indels: 55
DB:	3	Gaps: 8


```

; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328.352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 964
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-964

Alignment Scores:
Pred. No.: 0.047 Length: 1548
Score: 99.00 Matches: 60
Percent Similarity: 41.0% Conservative: 40
Best Local Similarity: 24.6% Mismatches: 94
Query Match: 6.4% Indels: 50
DB: 3 Gaps: 14

US-10-634-548-2 (1-304) x US-09-328-352-964 (1-1548)
Qy 7 LeuSerProIleAenHIGlnLeuCySarGpHeGlyAaAsnSerLeuThrHisArg 26
Db 67 CTCACCCCAATTAAAGTTAAATAGATGAAGAGCTTCATCTGCATTAATGCAAGCTG 126
Qy 27 PheCySerProGlyPheLeuIleSerProCySphIleGlyLeu---ThrGlyMet 45
Db 127 GCTTGTGAGACAAATGTGAATGAAGACAGCTACAGCTTACGGATTAATACAGCTTTT 186
Qy 46 Gly-----SerAlaThrGlnLeu-----ArgAlaArgSerLeu 57
Db 187 GCGTACTGCTTCACTCAATCAATGCGCGCTGAAAGATTGAAAAATTCACGGCTTCATTA 246
Qy 58 Ile---SerSerAlaValAlaIleThrAsnSerLeuHISerValGlyAlaThrValAla 76
Db 247 GTCTTGTGCATCGCGCAGGTGTAGGCGAAGACCTTGATGATGCAATGCTTCATTAAAT 306
Qy 77 ValIleGlyGlyAlaIleValAlaValLeuSerPheGluSerLeuThrIleArgAsnVal 96
Db 307 ATTCTATTGAAGCAAAATAGCTTGACAGTGTCTCTCGATAT---CGTCGTAAAGTC 363
Qy 97 IleGlnGlnSerLeu-----SerArgIleValAlaHisIle----- 108
Db 364 ATTGATGCTTGTGCGCTTAATTAATGCTGAAGTTTACCCACACATTCCACTTAAGGT 423
Qy 109 -----LeuSerGlyLeuLeuPheValLeuAlaIlePro-----IlePheSerGly 123
Db 424 TCAGTAGGGGCTTCTGGTGACTTGACACCCCTTGACACACATGCTTTGGTATTACTTGT 483
Qy 124 SerThrGluAlaArgIlePheAlaIlePheValProLeuValAsnGlyLeuArgSerVal 143
Db 484 GAAAGTAAAGCAGCTTAATGAAGTGAATGTTACACAGACAGTTGAAGCTTTAAATGCA 543
Qy 144 IleAsnGlyLeuSerIleSerProAsnSerMetLeuIleIleSerValIleThrArgGly 163
Db 544 -----GGTTTGAACCAATTTCTTTAGCGGCTTAA-----GAAAGT 579
Qy 164 ArgAlaGlnGluLeuLeuLeuGly-----ProLeuPheTyValLeuAlaLeuLeu 180
Db 580 TTGGCA-----CTTTTAATGTGTAACGAGTTTGACAGCTTACGCTTTACGTGGCTTA 633
Qy 181 PheSerAlaValPhePheTrpArgIleSerProIleGlyMetIleSerLeuAlaMetMet 200
Db 634 TTTGAAGACAGA-----GATTATTTGCTGCGCGACAGATT 669
Qy 201 CysGlyGlyAspGlyIleAlaAspIleMetGlyArgIlePheGlySerThrIleLeuPro 220
Db 670 TGTGTGTCTTAATGTTGAAGCAATGCTGTGT-----TCACGTGCACCT 714
Qy 221 TyrAsnProArg 224

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Db 715 TTGCATGGCGCT 726
RESULT 11
US-09-710-279-2167
; Sequence 2167, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/09/710.279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2167
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-2167

Alignment Scores:
Pred. No.: 0.0334 Length: 1152
Score: 98.50 Matches: 70
Percent Similarity: 40.9% Conservative: 58
Best Local Similarity: 22.4% Mismatches: 115
Query Match: 6.4% Indels: 71
DB: 3 Gaps: 13

US-10-634-548-2 (1-304) x US-09-710-279-2167 (1-1152)
Qy 13 GlnLeuCySarGpHeGlyAaAsnSerLeuThrHisArgPheCySerProGlyPhe 32
Db 181 CAATTCATGCTTTTAATATCAAGTACGTGCAAAATATTCATTTGAACA----- 231
Qy 33 LeuIleSerProCySphIleGlyLeuThrGlyMetGlySerAlaThrGlnLeuArg 52
Db 232 ATCATTTAGTATCA-----TGGTGACTGTTTAAAGTCAAGCATATTAATTG 282
Qy 53 AlaArgSerLeuIleSerSerAlaValAlaIleThrAsnSerLeuHISerValGly 72
Db 283 ATTAACAATGTAAATTTATGTTAGTGTGAAAAAGT-----TTAGAAAAAGCTTCT 336
Qy 73 AlaThrValAlaValAlaValGlyAlaIleValAlaValLeuSerPheGluSerLeuThr 92
Db 337 AAAATTAATGATGCTCTAATTAATTAATCTTTTAATATCGTTGACACAAATCTTAAC 396
Qy 93 LysArgAsnValIleGln-----GlnSerLeuSer 102
Db 397 TTAGAAGTGCTTTTGAAGAGGTGATATATATCTGAACCTCGAGTTGAAGATGCT 456
Qy 103 ArgIleLeuValHisIleLeuSerGlyLeuLeuPheValLeuAlaIleProIlePheSer 122
Db 457 -----ATTCAGAGGTGATCTAATTTATGTTGGGTGACACAAATCGTTTAAAG 498
Qy 123 -----GlySerThrGluAlaArgIlePheAlaIlePheValPro----- 135
Db 499 CTGTCCTAGGTACACCGGAATATTAATTAATGACCTTAATAAATATGACG 558
Qy 136 -----LeuValAsnGlyLeuArgLeuValIleAsnGly 146
Db 559 ATAAAGTCTTCAGACATTTCATTTGCGTAATGAATATTTTAATTTCTGTGCTGCGGA 618
Qy 147 LeuSerIleSerProAsnSerMetLeuIleIleSerValIleThrArgGlnGlyArgAlaGlu 166
Db 619 TTACCTTAATTTCTTGGCGCTTAATAACATTTGGTTACCAACCCCAAGAGG----- 669
Qy 167 GluLeuLeuGlyGlyProLeuPheTyValLeuAlaLeuLeuPheSerAlaValPhePhe 186

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Db      670 -----CCTGGCTTATTATTTAGAGTTTACCACTAGATTTAGCGGAATGAC-TTT 719
Qy      187 TTPARGUSERPROILEGLYMETILSERLEUALMETCYGGLYASP-GLY11 206
Db      720 TGGTACATCTTTTACTTATTTTACTATTTATTTATTTGGGCAATTGACCTTTC 779
Qy      206 eAlaSerIleMetGlyArgLysPheGlySer---ThiLysIleProTyrAnProArgLy 225
Db      780 TATATCATATTATAGAGTTAAATGTCATATTTTCAATTTTCAAAAATGATAATAGTAAAGCA 839
Qy      225 sSerTrpAla-----GlySerIleSerMetPheIlePheGlyPhePheIleSerIleAl 243
Db      840 AAAAGTGCACATCATAGAGTACTGATATTCTGATTTATTC-----ATTAGTATCCC 887
Qy      243 aleuLeuLeuYrTyrIleSerSerLeuGlyTyrLeuHisMetLeuTrpGluThrLeuGl 263
Db      888 AGCAACATTATCTTTTATAGTCTAATGTCATTTGCGTTTGGC----- 930
Qy      263 nArgValAlaMetValSerMetValAlaThrValValGluSerLeuProIleThrAspGl 283
Db      931 -----GCTGTCACATATTGATATATAG-----GATTT 959
Qy      283 nLeuAspAspAsnIleSerValProLeuAlaThrIle 295
Db      960 TATTGTATCTAATATTCTTATGTCATTTAGGGGCACCTA 996

RESULT 12
US-09-134-001C-1098
; Sequence 1098, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lydn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1098
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1098

Alignment Scores:
Pred. No.: 0.0439      Length: 1359
Score: 98.50          Matches: 70
Percent Similarity: 40.9%      Conservative: 58
Best Local Similarity: 22.4%      Mismatches: 115
Query Match: 6.4%          Indels: 71
DB: 3                  Gaps: 13

US-10-634-548-2 (1-304) x US-09-134-001C-1098 (1-1359)
Qy      13 GlnLeuCyArgPheGlyAsnAsnSerLeuThrThrHisArgPheCySerProGlyPhe 32
Db      388 CAATCATGTTTAAATCAAGTACGCTGACAAATATTCATTTGAACA----- 438
Qy      33 LeuIleSerSerProCyAspHeIleGlyLeuThrGlyMetGlySerAlaThrGlnLeuArg 52
Db      439 ATCATTTGTTTATCA-----TGTGACCTGTTTATGCTCAAGCGCATTTATTG 489
Qy      53 AlaArgSerLeuLeuSerSerSerAlaValAlaThrAsnSerLeuLeuHisAspValGly 72
Db      490 ATTAACAATGTAATTGTATGTTAGCTGTTGAAAAAGG-----TTAGAAAAAGCTTCT 543
Qy      73 AlaThrValAlaValLeuGlyGlyAlaTyrAlaLeuValLeuSerPheGluSerLeuThr 92

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Db      544 AAAATTAATGATGCTCTATATTTATTTATCTTTTAAATATCGTTGAGCAATCTTTACT 603
Qy      93 LysArgAsnValIleGln-----GlnSerLeuSer 102
Db      604 TTGAAAGTGCTTTAGAAAGTGTCATATATATCTGCAACCTGAGTTGAAGATATGCT 663
Qy      103 ArgLysLeuValHisIleLeuSerGlyLeuLeuPheValLeuAlaTrpProIlePheSer 122
Db      664 -----ATTCAGAGTGATCTATTTTCGTTAGGGCAATCGTTTATACG 705
Qy      123 -----GlySerThrGluAlaArgTyrPheAlaIlePheValPro----- 135
Db      706 CTGTCCTTAGTACACCGGATGATATCTTATGCAAGCTTATGCACTTAAAAATATGACG 765
Qy      136 -----LeuValAsnGlyLeuArgLeuValIleAsnGly 146
Db      766 ATTAAGCTTTCAGACATTTCAATTGTGTGTAATGAATTTTAATTTCTGTGCTGGCTGCA 825
Qy      147 LeuSerIleSerProAsnSerMetLeuIleLysSerValThrArgGluGlyArgAlaGlu 166
Db      826 TTACCTATATTCTTCCGCGCTTAAACATTTGGTTACCAACCCCAAGAGGC----- 876
Qy      167 GluLeuLeuYsGlyProLeuPheTyrValLeuAlaLeuLeuPheSerAlaValPhePhe 186
Db      877 -----CCTGCTTATTTATTTAGAGTCTTACCACTAGATTTTACGGAATGAC-TTT 926
Qy      187 TTPARGUSERPROILEGLYMETILSERLEUALMETCYGGLYASP-GLY11 206
Db      927 TGGTACATCTTTTACTTATTTATTTTACTATTTATTTATTTGCGGCAATTAAGCTTTC 986
Qy      206 eAlaAspIleMetGlyArgLysPheGlySer---ThiLysIleProTyrAnProArgLy 225
Db      987 TATATCATTTATTAAGTAAATGTCATCTAATTTTATCTAATAAATGATAATAGTAAAGCA 1046
Qy      225 sSerTrpAla-----GlySerIleSerMetPheIlePheGlyPhePheIleSerIleAl 243
Db      1047 AAAAGTGCACATCATAGAGTACTGATATTATTC-----ATTAGTATCCC 1094
Qy      243 aleuLeuLeuYrTyrIleSerSerLeuGlyTyrLeuHisMetLeuTrpGluThrLeuGl 263
Db      1095 AGCAACATTATCTTTTATGATCTTATGACATTTGCGTTTGGC----- 1137
Qy      263 nArgValAlaMetValSerMetValAlaThrValValGluSerLeuProIleThrAspGl 283
Db      1138 -----GCTGTCACATATTGATATATAG-----GATTT 1166
Qy      283 nLeuAspAspAsnIleSerValProLeuAlaThrIle 295
Db      1167 TATTGTATCTAATATTCTTATGTCATTTAGGGGCACCTA 1203

RESULT 13
US-09-710-279-3427/C
; Sequence 3427, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P0348005
; CURRENT APPLICATION NUMBER: US/09/710,279
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3427
; LENGTH: 3108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-3427

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Alignment Scores:

Pred. No.:	0.171	Length:	3108
Score:	98.50	Matches:	70
Percent Similarity:	40.9%	Conservative:	58
Best Local Similarity:	22.4%	Mismatches:	115
Query Match:	6.4%	Indels:	71
		Gaps:	13

US-10-634-548-2 (1-304) x US-09-710-279-3427 (1-3108)

```

Qy      13 GlnLeuCyArgPheGlyAsnAsnSerLeuThrH1sArgPheCySerProGlyPhe 32
Db      3087 CAATCAAGCTTTTAAATCAAGTACCTGACCAATATTCATTTGAACA----- 3037
Qy      33 LeuLeuSerSerProCyPheHelLeuThrGlyMetGlySerAlaThrGlnLeuArg 52
Db      3036 ATCATTAAGTATATCC-----TGGTGAAGCTTTTAAAGTCAGCAAGCATTTATTTG 2986
Qy      53 AlaArgArgSerLeuLeuSerSerAlaValAlaThrAsnSerLeuLeuHisArgValGly 72
Db      2985 ATTAACAATGATATTGTTATGTTAGCTTTGAAAAAGCT-----TTAGAAAAAGCTTCT 2932
Qy      73 AlaThrValAlaValLeuGlyGlyAlaTyraAlaLeuValLeuSerPheGlnSerLeuThr 92
Db      2931 AAAATTAATGATGCCCTCTATTATTTATCTTTTAATATCGTGTAGCAATCTTTAACT 2872
Qy      93 LysArgAsnValIleGln-----GlnSerLeuSer 102
Db      2871 TTAGAAAGGTGCTTTAGAAAGGTGTCATTAATTAATCTGCAACCTCGAGTTGAAGATGTGCT 2812
Qy      103 ArgLysLeuValHisIleLeuSerGlyLeuLeuPheValLeuAlaThrProIlePheSer 122
Db      2811 -----ATTCAGGTGATCTATTGCGTTAGCAATCGCTTTTACG 2770
Qy      123 -----GlySerThrGlnAlaArgTyraPheAlaAlaPheValPro----- 135
Db      2769 CTGTCCTAGGTGACACCGAATGATTAATGACAGTATGACACCTGCTGCTGCTGCTGCA 2710
Qy      136 -----LeuValaGlnGlyLeuArgLeuValIleAsnGly 146
Db      2709 ATAAAGTCTTGACACTTTCAATTCGTAAATGAATATTTAATTTCTGCTGCTGCTGCA 2650
Qy      147 LeuSerIleSerProAsnSerMetLeuLeuSerValThrArgGlnGlyArgAlaGln 166
Db      2649 TTAGCTATTATTTCTGCGCTTAAACATTTGGTTACCAACCCCAAGAGGC----- 2599
Qy      167 GluLeuLeuGlyGlyProLeuPheTyraValLeuAlaLeuLeuPheSerAlaValPhePhe 186
Db      2598 -----CCGGCTTATTATTAAAGTTTAAACCACTAGTATTAGGGAATAGC-TTT 2549
Qy      187 TrpArgGlnSerProIleGlyMetIleSerLeuAlaMetMetCyGlyGlyAsp-GlyI1 206
Db      2548 TGGTACATCTTTTCACTTAATTTTACTATTATTTGCGGCACTTAACCTCTTC 2489
Qy      206 AlaAspIleMetGlyArgLysPheGlySer---ThrLysIleProTyraAsnProArgLys 225
Db      2488 TATATCATTAATTAAGTAAATGTAATTTTCTAAATTTTCTAAATAATGTAATAAAGCA 2429
Qy      225 sSerTrpAla-----GlySerIleSerMetPheIlePheGlyPhePheIleSerIleAl 243
Db      2428 AAAAGTGCATTCATAGGTAGTATGTAATCTGTAATTATC-----ATTAGTATCC 2381
Qy      243 AlaLeuLeuTyraTyraSerSerLeuGlyTyraLeuHisMetAsnTrpGlnThrLeuGln 263
Db      2380 AGCAACATTAATCTTTTATGATGTAAGTCATTTGGTGGT----- 2338
Qy      263 nArgValAlaMetValSerMetValAlaThrValAlaGlnSerLeuProIleThrAspGln 283
Db      2337 -----GCTGTAACGATATTGATTAATATG-----GATTT 2309
Qy      283 nLeuAspAsnAsnIleSerValProLeuAlaThrIle 295
Db      2308 TATGTATCATTAATTTCTTATGCGCATTTAGGGGCACTA 2272

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RESULT 14

US-09-543-681A-282

; Sequence 282, Application US/09543681A

; Patent No. 6605709

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543,681A

; PRIOR FILING DATE: 2000-04-05

; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 282

; LENGTH: 903

; TYPE: DNA

; ORGANISM: Proteus mirabilis

US-10-634-548-2 (1-304) x US-09-543-681A-282 (1-903)

Alignment Scores:

Pred. No.:	0.03	Length:	903
Score:	97.50	Matches:	66
Percent Similarity:	39.2%	Conservative:	38
Best Local Similarity:	24.9%	Mismatches:	78
Query Match:	6.3%	Indels:	83
		Gaps:	17

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Qy      31 GlyPheLeuLeuLeuSerSerProCyPheHelLeuThrGlyMetGlySerAlaThrGln 50
Db      214 GGTATTATCTCTCC-----AGATCATATATGGA-----ACCCCA 249
Qy      51 LeuArgAlaArgArgSerLeuLeuSerSerAlaValAlaThrAsnSerLeuLeuHisAsp 70
Db      250 ATGCGTGCCTTAATCTCTTTATC-----CGTTGGCTCATTCATTAATGATGA 303
Qy      71 Val-----GlyAlaThrValAlaValLeuGlyGlyAlaTyraAlaLeuValLeuSerPhe 88
Db      304 ATGCAAGTGTGTCACACTCTTTGCTTATGCTGCTTATATGCTTAAT----- 354
Qy      89 GluSerLeuThrLysArgAsnValIleGlnGlnSerLeuSerArgLysLeuValHisIle 108
Db      355 AGTGTATTAATTAATTAATGCGCGCTGCAATTAATTTGCTAGTGTGTCATGATTA 414
Qy      109 LeuSerGlyLeuLeuPheValLeuAla----- 117
Db      415 CTTCGA---GTGCTATTATTAACGGCTATTTCGCGAGTTTATCAATTAATGATACGTACT 471
Qy      118 ---TrpProIlePheSerGlySerThrGlnAlaArgTyra---PheAlaAlaPheVal--- 134
Db      472 ACTTGG-----TATTAATGCTATTAACCACTTAATCTGCTAATCAACGCTTATTTGGC 525
Qy      135 ---ProLeuValaGlnGlyLeuArgLeuValIleAsnGlyLeuSerIleSerProAsnSer 153
Db      526 GGCCTATTATTAAGCGGCACTGTAATGCGTATTCGCGGTTTAACTTAATTAATGATTA 585
Qy      154 MetLeuLeuLysSerValThrArgGlnGlyArgAlaGlnGlnLeuLeuGlyGlyProLeu 173
Db      586 GCATTA-----CCGCTA 597
Qy      174 PheTyraValLeuAlaLeuLeuPheSerAlaValaPhePheTrpArgGlnSer---ProIle 192
Db      598 TTAAGTGCATCGCATTAATATATCAATGCTATTGTGCTACCTCAAGCGCTTGAATTA 657
Qy      193 GlyMetIleSerLeuAlaMetMetCyGlyGlyArgGlyIleAlaAsp-----Ile 209
Db      658 GTTCAATTAACCTCGTACCAAAAAGCGGTGATTAATTAATTAATTAATTAATTAATTA 717
Qy      210 MetGlyArgLysPheGlySerThrLysIle----- 219

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Db      718 ATGGGCAATTAATGATTCGCCCTAATAGGAGTTAGCTGTGATAGACACCGTTATTA 777
Qy      220 ---ProTyrAnProArgLysSerTrpAlaGlySerIleSerMetPheIlePhe 238
Db      778 CGCAAAATAATATCC-----TCGTGTTCTTTAATAGTGTGTAGTTT 819
Qy      239 -----PheIleSerIleAlaLeuLeuTyrTyrTyrSerSerLeu 251
Db      820 ATTTGGCTTTGTTGTCGATTTATTTGTCGTGCGCATTCCTA----- 864
Qy      252 GlyTyrLeuHisMet 256
Db      865 ---GGCTTACATATG 876

RESULT 15
US-09-543-681A-650
; Sequence 650, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 650
; LENGTH: 1227
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-650

Alignment Scores:
Pred. No.: 0.0575      Length: 1227
Score: 97.00          Matches: 59
Percent Similarity: 36.5%      Conservative: 54
Best Local Similarity: 19.0%      Mismatches: 106
Query Match: 6.3%          Indels: 91
DB: 3                  Gaps: 11

US-10-634-548-2 (1-304) x US-09-543-681A-650 (1-1227)
Qy      10 ILeaenHisGlnLeuCyArgPheGlyAenAenSerLeuThr-----HisArg 26
Db      300 TTGGGTAGACAGTGTGCGGTTTACTAACAGCGCTTTTACAAAGCTTTGGCGTCTG 359
Qy      27 PheCySerProGlyPheLeuIleSerSerProCyPheIleGlyLeuThrGly-MetG1 46
Db      360 CTCCTCAGCCGT-----TATTTGCCAAGCAGCTAGTATAGA 395
Qy      46 ySerAlaThrGlnLeuArgAlaArgArg-----SerLeuIleSerSerAlaValAl 63
Db      396 CGGTTTGTAGTGTGCGGCTCAGCAACACGTTTTCGCATCATATATGTCATGCGCCCT 455
Qy      63 eThzAenSerLeuLeuHisArgValGlyAlaThrValAlaValLeuGlyGly----- 80
Db      456 TTCCCGACGCTTAGCGGCACTCATTTGCTCTTTCTGTTAAACACAGGAGGCGGCGCAT 515
Qy      81 -----AlaTyrAlaLeuValIleuSerPheGluSerLeuThrLysArg 94
Db      516 GATCTTTATGTTGTCGATGCGCAATTACTCTTGTATTATATGCTAACCCACATGATGCTAA 575
Qy      94 gAnValAlIleGlnIleSerLeuSerArgLysLeuValHisIleLeuSerGlyLeuLeuPh 114
Db      576 AAATATTAACAATAATCAGTTATGATGACAGGCCCATCTACAGTATCA---TTTTTAAC 632
Qy      114 eValIleuAlaTProIlePheSerGlySer-----ThrGluAlaArgTyrPheAlaAl 132
Db      633 TTTCCTTAAGTACCTTAATGCCGAGTAACGATTAATGTTTACGCGTCTGTAAGTCCGGG 692
Qy      132 apHeValProLeuValaenGlyLeuArgLeuValIleAenGlyLeuSerIleSerProAs 152

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Db      693 TTTCTTGTGCTTGTAGACAGGCTCTCCGATTAATCTTGAGAAGATGGCTTATTTACACACA 752
Qy      152 nSerMetLeuIleLysSerValThrArgGluGlyArgAlaGluGluLeuLysGlyPr 172
Db      753 AGATATCGGCTTAAGCTATATTTCCAA----- 780
Qy      172 OleuPheTyrValLeuAlaLeuLeuPheSerAlaValPhePheTrpArgLysProI1 192
Db      780 ----- 780
Qy      192 eGlyMetIleSerLeuAlaMetMetCysGlyGlyAspGlyTyrIleAlaAspIleMetGlyAr 212
Db      781 -----ACCATCGCATTTATGTAAGGTGTTATGTTGTCGCATTCATTAATTCAAA 830
Qy      212 GlyPheGlySerThrLysIleProTyrAnProArgLysSerTrpAlaGlySerIleSe 232
Db      831 AATGTCGGGTAAACACTGTATCCT----- 855
Qy      232 rMetPheIlePheGlyPhePheIleSerIleAlaLeuLeuTyrTyrTyrSerSerLeuG1 252
Db      856 -TTATGTTATTTGCTTACGACGATGACAGCGTGTGTTCTTAATGTCGCAAA----- 909
Qy      252 YTyLeuHisMetAsnTrpGluThrThrLeuGlnArgValAlaMetValSerMetValAl 272
Db      910 -TATACACACCCCAACATTAAACAAATTTTATTCATTTGTATTTATGATGCGTGTATG-- 966
Qy      272 aThrValValLysLeuProIleThrAspGlnLeuAspAenIleSerValProLe 292
Db      967 -----AACGGTCTTCTTAATCCAT 986
Qy      292 uAla-----ThrIleLeuAlaAlaTyr 299
Db      987 TGCTGTCTTAATGCGCTATCAGGCTAC 1014

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Search completed: March 16, 2006, 23:47:52
Job time : 1016 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 16, 2006, 23:30:08 ; Search time 904 Seconds
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2780.853 Million cell updates/sec

Title: US-10-634-548-2

Perfect score: 1536
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-YGAOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1536	100.0	1015	7	US-10-425-114-21028
2	1536	100.0	1091	7	US-10-634-548-1
3	1523	99.2	980	7	US-10-425-114-14606
4	1284.5	83.6	1897	7	US-10-634-548-3
5	1266	82.4	1062	7	US-10-425-114-29129
6	870	56.6	1007	7	US-10-425-114-20410
7	794	51.7	1085	7	US-10-425-114-22326

8	794	51.7	1974	7	US-10-437-963-77300	Sequence 77300, A
9	794	51.7	2514	7 <td>US-10-437-963-77301</td> <td>Sequence 77301, A</td>	US-10-437-963-77301	Sequence 77301, A
10	788	51.3	1103	7 <td>US-10-425-114-26593</td> <td>Sequence 26593, A</td>	US-10-425-114-26593	Sequence 26593, A
11	777	50.6	1123	8 <td>US-10-425-115-118753</td> <td>Sequence 118753, A</td>	US-10-425-115-118753	Sequence 118753, A
12	776	50.5	798	7 <td>US-10-425-114-23255</td> <td>Sequence 23255, A</td>	US-10-425-114-23255	Sequence 23255, A
13	773	50.3	976	7 <td>US-10-425-114-26551</td> <td>Sequence 26551, A</td>	US-10-425-114-26551	Sequence 26551, A
14	751	48.9	723	7 <td>US-10-425-114-25671</td> <td>Sequence 25671, A</td>	US-10-425-114-25671	Sequence 25671, A
15	751	48.9	753	7 <td>US-10-425-114-26498</td> <td>Sequence 26498, A</td>	US-10-425-114-26498	Sequence 26498, A
16	742	48.3	937	7 <td>US-10-425-114-26454</td> <td>Sequence 26454, A</td>	US-10-425-114-26454	Sequence 26454, A
17	646	42.1	674	7 <td>US-10-425-114-16877</td> <td>Sequence 16877, A</td>	US-10-425-114-16877	Sequence 16877, A
18	594	38.7	992	7 <td>US-10-424-599-112249</td> <td>Sequence 112249, A</td>	US-10-424-599-112249	Sequence 112249, A
19	574.5	37.4	1286	8 <td>US-10-425-115-172503</td> <td>Sequence 172503, A</td>	US-10-425-115-172503	Sequence 172503, A
20	573	37.3	916	8 <td>US-10-739-930-1001</td> <td>Sequence 3001, Ap</td>	US-10-739-930-1001	Sequence 3001, Ap
21	572.5	37.3	1225	7 <td>US-10-425-114-26462</td> <td>Sequence 26462, A</td>	US-10-425-114-26462	Sequence 26462, A
22	567.5	36.9	688	7 <td>US-10-425-114-22387</td> <td>Sequence 22387, A</td>	US-10-425-114-22387	Sequence 22387, A
23	567.5	36.9	907	7 <td>US-10-767-701-11210</td> <td>Sequence 11210, A</td>	US-10-767-701-11210	Sequence 11210, A
24	566.5	36.9	666	7 <td>US-10-425-114-4925</td> <td>Sequence 4925, Ap</td>	US-10-425-114-4925	Sequence 4925, Ap
25	566.5	36.9	955	8 <td>US-10-425-115-118754</td> <td>Sequence 118754, A</td>	US-10-425-115-118754	Sequence 118754, A
26	552.5	36.0	1091	7 <td>US-10-425-114-26298</td> <td>Sequence 26298, A</td>	US-10-425-114-26298	Sequence 26298, A
27	545.5	35.5	1241	8 <td>US-10-739-930-4866</td> <td>Sequence 4866, Ap</td>	US-10-739-930-4866	Sequence 4866, Ap
28	544.5	35.4	1430	8 <td>US-10-424-599-11025</td> <td>Sequence 71025, A</td>	US-10-424-599-11025	Sequence 71025, A
29	540.5	35.2	795	7 <td>US-10-425-114-13412</td> <td>Sequence 13412, A</td>	US-10-425-114-13412	Sequence 13412, A
30	539	35.1	867	7 <td>US-10-425-114-25373</td> <td>Sequence 25373, A</td>	US-10-425-114-25373	Sequence 25373, A
31	536.5	34.9	1046	7 <td>US-10-425-114-19295</td> <td>Sequence 19295, A</td>	US-10-425-114-19295	Sequence 19295, A
32	530.5	34.5	1162	7 <td>US-10-634-548-5</td> <td>Sequence 5, Appli</td>	US-10-634-548-5	Sequence 5, Appli
33	529	34.4	1057	7 <td>US-10-767-701-11766</td> <td>Sequence 11766, A</td>	US-10-767-701-11766	Sequence 11766, A
34	517	33.7	876	7 <td>US-10-437-963-97687</td> <td>Sequence 97687, A</td>	US-10-437-963-97687	Sequence 97687, A
35	517	33.7	1193	8 <td>US-10-739-930-1297</td> <td>Sequence 1297, Ap</td>	US-10-739-930-1297	Sequence 1297, Ap
36	517	33.7	1281	7 <td>US-10-767-701-11596</td> <td>Sequence 11596, A</td>	US-10-767-701-11596	Sequence 11596, A
37	512	33.3	1029	7 <td>US-10-425-114-14899</td> <td>Sequence 14899, A</td>	US-10-425-114-14899	Sequence 14899, A
38	511.5	33.3	648	7 <td>US-10-425-114-16929</td> <td>Sequence 16929, A</td>	US-10-425-114-16929	Sequence 16929, A
39	509	33.1	944	7 <td>US-10-425-114-19979</td> <td>Sequence 19979, A</td>	US-10-425-114-19979	Sequence 19979, A
40	509	33.1	1106	7 <td>US-10-425-114-28780</td> <td>Sequence 28780, A</td>	US-10-425-114-28780	Sequence 28780, A
41	508	33.1	948	7 <td>US-10-425-114-19980</td> <td>Sequence 19980, A</td>	US-10-425-114-19980	Sequence 19980, A
42	500.5	32.6	818	7 <td>US-10-437-963-38063</td> <td>Sequence 38063, A</td>	US-10-437-963-38063	Sequence 38063, A
43	490	31.9	1044	7 <td>US-10-425-114-26552</td> <td>Sequence 26552, A</td>	US-10-425-114-26552	Sequence 26552, A
44	486.5	31.7	1548	8 <td>US-10-425-115-44228</td> <td>Sequence 54228, A</td>	US-10-425-115-44228	Sequence 54228, A
45	483	31.4	1086	7 <td>US-10-767-701-11767</td> <td>Sequence 11767, A</td>	US-10-767-701-11767	Sequence 11767, A

ALIGNMENTS

RESULT 1
US-10-425-114-21028
; Sequence 21028, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 21028
; LENGTH: 1015
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana columbia
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3278-077-D5_FLI
US-10-425-114-21028
Alignment Scores:
Pred. No.: 1.66e-177
Score: 1536.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
Length: 1015
Matches: 304
Conservative: 0
Mismatch: 0
Indels: 0

DB: 7 Gaps: 0
US-10-634-548-2 (1-304) x US-10-425-114-21028 (1-1015)
QY 1 MetAlaAlaThrLeuProLeuSerProIlleAenHlsgInLeuCyAaXpHeGlyAaenAn 20
DB 35 ATGGAGCAACCTTACTCTATCTCCGATCAATCATAGTGTGTGGTCCGGAAACAC 94
QY 21 SerLeuThrThrHlaAaXpHeCySerProGlyPheLeuIlleSerSerProCyAaHeIlle 40
DB 95 TCTTTGACGACCTACCGGCTTCTGTCTCTCCGCTTCTGTATCTTCTCTGTTTCAT 154
QY 41 GlyLeuThrGlyMeGlySerAlaThrGlnLeuAaGlaAaXpSerLeuIlleSerSer 60
DB 155 GGTGGACCGGAATGGGCTCTCTACTAGTACGTGCTCGTCTCTGATCTCTTCA 214
QY 61 AlaValAlaThrAaenSerLeuLeuHlAaPValGlyAlaThrValAlaValLeuGlyGly 80
DB 215 GCAGTTGCGACGAATTCGCTGTGTGATGACGTCCGAGCCACCGTGGCAGTCTGTGGA 274
QY 81 AlaTyrAlaLeuValLeuSerPheGlyLeuThrLyAaXpAaenValIlleGlnGlnSer 100
DB 275 GCATACGGCGCTGTCTTAAGCTTCAAGATCTCACCAAGCCGAAGCTCATCAACAGAGT 334
QY 101 LeuSerAaGlyAaLeuValHlIlleLeuSerGlyLeuLeuPheValLeuAlaTrrProIlle 120
DB 335 TTGACCAAGAACTTGTGATATCTCTCAGGCTCTGCTTTCTGATCTTGGCCCAATC 394
QY 121 PheSerGlySerThrGlnAlaAaGlyrPheAlaAlaPheValProLeuValAaenGlyLeu 140
DB 395 TTCACGGATCGACCGAGGCTCGATACCTTTCGCTTTGTTCCGTATGATGAGCTTA 454
QY 141 ArgLeuValIlleAaenGlyLeuSerIlleSerProAaenSerMetLeuIlleYSerValThr 160
DB 455 AGCGTTGTATTAAACGACTATCCATTTCCCAATTCATCTCAATCAATCCGTCACA 514
QY 161 ArgGlnGlyArgAlaGlnGlnLeuLeuGlyGlyProLeuPheThrValLeuAlaLeuLeu 180
DB 515 AAGAGAGGAGAGAGAGAGAGTTCCTTAAGGTCCTTGTCTCAAGCTTACTCTTCTT 574
QY 181 PheSerAlaValPhePheTrrPArgIuserProIlleGlyMeCllleSerLeuAlaMetMet 200
DB 575 TTCCTGCGCGTTTCTTCTGAGAGAGTCTCTATCGGTATGATCTCGTTACCAATGATG 634
QY 201 CyAaGlyAaPBGlyrIlleAlaAaPllleMetGlyAaXpAaPheGlySerThrLyAaIllePro 220
DB 635 TGTGTGGCGGATGAAATAGCTGATATATATGAGAGCTTGGGTCATCACTAAGATACCT 694
QY 221 TyrAaenProAaGlySerTrrPAlaGlySerIlleSerMetPheIllePheGlyPhePheIlle 240
DB 695 TACAACCCAGAGAGAGAGTGGGCGAGAGACATCTCCATCTTCACTTGGCTTCTTCACT 754
QY 241 SerIlleAlaLeuLeuTyrTrrTyrSerSerLeuGlyTrrLeuHlAaMetAaenTrrPArgIuser 260
DB 755 TCCATCGCATCTTACTTACTTACTCAACCTTGGGTACTTCACTCACTGAGGAAAG 814
QY 261 ThrLeuGlnAaValAlaMetValSerMetValAlaThrValAaGlnSerLeuProIlle 280
DB 815 ACCCTTGCAAGAGTACCAATGGCTCAATGGTCCAGGAGTACAGTACAGTACCCATC 874
QY 281 ThrAaPBGlnLeuAaPBGlnIlleSerValProLeuAlaThrIlleLeuAlaAlaTrrLeu 300
DB 875 ACCGATCATTTAGACACAAATATTTGGTTCCTGCGTACATATTTTACTGCTTATTTA 934
QY 301 SerPheGlyTrr 304
DB 935 AGTTTCGATAT 946

RESULT 2
US-10-634-548-1
; Sequence 1, Application US/10634548
; Publication No. US20040045051A1
; GENERAL INFORMATION:

; APPLICANT: No. US20040045051A1tris, Susan R
; APPLICANT: Lincoln, Kim
; APPLICANT: Abad, Mark Scott
; APPLICANT: Eilers, Robert
; APPLICANT: Hartsuiker, Karen Kindie
; APPLICANT: Hirschberg, Joseph
; APPLICANT: Karunanandaa, Balasulojini
; APPLICANT: Moshiri, Farhad
; APPLICANT: Stein, Joshua C.
; APPLICANT: Valentin, Henry B.
; APPLICANT: Venkatesh, Tyamgondlu V.
; TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof
; FILE REFERENCE: Ren-01-125
; CURRENT APPLICATION NUMBER: US/10/634, 548
; PRIOR FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: us 60/400,689
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1091
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-634-548-1
Alignment Scores:
Pred. No.: 1,866-177 Length: 1091
Score: 1536.00 Matches: 304
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
Query Match: 7 Gaps: 0
DB: 7
US-10-634-548-2 (1-304) x US-10-634-548-1 (1-1091)
QY 1 MetAlaAlaThrLeuProLeuSerProIlleAenHlsgInLeuCyAaXpHeGlyAaenAn 20
DB 108 ATGGAGCAACCTTACTCTATCTCCGATCAATCATAGTGTGTGGTCCGGAAACAC 167
QY 21 SerLeuThrThrHlaAaXpHeCySerProGlyPheLeuIlleSerSerProCyAaHeIlle 40
DB 168 TCTTTGACGACCTACCGGCTTCTGTCTCTCCGCTTCTGATCTTCTCTGTTTCAT 227
QY 41 GlyLeuThrGlyMeGlySerAlaThrGlnLeuAaGlaAaXpSerLeuIlleSerSer 60
DB 228 GGTGGACCGGAATGGGCTCTCTACTAGTACGTGCTCGTCTCTGATCTCTTCA 287
QY 61 AlaValAlaThrAaenSerLeuLeuHlAaPValGlyAlaThrValAlaValLeuGlyGly 80
DB 288 GCAGTTGCGACGAATTCGCTGTGTGATGACGTCCGAGCCACCGTGGCAGTCTGTGGA 347
QY 81 AlaTyrAlaLeuValLeuSerPheGlyLeuThrLyAaXpAaenValIlleGlnGlnSer 100
DB 348 GCATACGGCGCTGTCTTAAGCTTCAAGATCTCACCAAGCCGAAGCTCATCAACAGAGT 407
QY 101 LeuSerAaGlyAaLeuValHlIlleLeuSerGlyLeuLeuPheValLeuAlaTrrProIlle 120
DB 408 TTGACCAAGAACTTGTGATATCTCTCAGGCTCTGCTTTCTGATCTTGGCCCAATC 467
QY 121 PheSerGlySerThrGlnAlaAaGlyrPheAlaAlaPheValProLeuValAaenGlyLeu 140
DB 468 TTCACGGATCGACCGAGGCTCGATACCTTTCGCTTTGTTCCGTATGATGAGCTTA 527
QY 141 ArgLeuValIlleAaenGlyLeuSerIlleSerProAaenSerMetLeuIlleYSerValThr 160
DB 528 AGCGTTGTATTAAACGACTATCCATTTCCCAATTCATCTCAATCCGTCACA 587
QY 161 ArgGlnGlyArgAlaGlnGlnLeuLeuGlyGlyProLeuPheThrValLeuAlaLeuLeu 180
DB 588 AAGAGAGGAGAGAGAGAGTTCCTTAAGGTCCTTGTCTTCAAGCTTCAAGCTTCTT 647
QY 181 PheSerAlaValPhePheTrrPArgIuserProIlleGlyMeCllleSerLeuAlaMetMet 200

PRIOR APPLICATION NUMBER: US 60/400,689

PRIOR FILING DATE: 2002-08-05
 NUMBER OF SEQ ID NOS: 79
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 3
 LENGTH: 1897
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 US-10-634-548-3

Alignment Scores:

Pred. No.:	3,226-146	Length:	1897
Score:	1284.50	Matches:	301
Percent Similarity:	52.4%	Conservative:	0
Best Local Similarity:	52.4%	Mismatches:	3
Query Match:	83.6%	Indels:	272
DB:	7	Gaps:	5

US-10-634-548-2 (1-304) x US-10-634-548-3 (1-1897)

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QY      1 MetAlaIaThrLeuProLeuSerProIleAenHsGInLeuCyArgPheGlyAsnAsn 20
DB      108 ATGGACGACCTTACCTCTATCTCGATCAATCATAGTTGTGCGGTGGGAACAC 167
QY      21 SerLeuThrThrHisArgPheCySerProGlyPheLeuIleSerSerProCyAspHeIle 40
DB      168 TCTTTGACGACTCACCGTTCGTCTCTCGCTTCCTGATTTCTTCTCTGTTTCATT 227
QY      41 GlyLeuThrGlyMetGlySerAlaThrGlnLeuArgAlaArgArgSerLeuIleSerSer 60
DB      228 GGTGTGACCGGAAATGGGCTGTGCTACTCAGTTACGTCGTCGTCCTGATCTCTCA 287
QY      61 AlaValAlaThrAsnSerLeuLeuHisAspValGlyAlaThrValAlaValLeuGly 80
DB      288 GCAAGTTGCAACAATTCCTGTGTCATGACGTCGAGCCACCGTGGCAGCTGTGTGGA 347
QY      81 AlaTyraIaLeuValLeuSerPheGlnSerLeuThrTyraArgAsnValIleGln----- 98
DB      348 GCATACGGCGCTGTCTTAAGCTTCGAGAGTCCACCAAGCGAAACGTCAATCAACAGGTC 407
QY      98 ----- 98
DB      408 TCTTAATAATCGTTTAACTTATCCACAACAATTCCTCGTTTACAATTCAGTTTATTCG 467
QY      98 ----- 98
DB      468 AACACCACTATATGTTGAAAGAAGTTCTCAAGTTGTGTTGACAGTACTCATTAGAA 527
QY      98 ----- 98
DB      528 ACAATGATTAAGCCTAGAAATTTGTGTGAATTAATTTTCAATTCGAATTTTATTA 587
QY      98 ----- 98
DB      588 GAATTTGTAACACTTAGTAAGCAGTAATCACTTATCATGACCAATCGTAAGACGGA 647
QY      98 ----- 98
DB      648 CAAGAACAAGTGTCCAAAATATTTACCGCTTATATATGTTACCACTTTCTTAACCTC 707
QY      98 ----- 98
DB      708 CCTTTAACTATCCGTAATCGCTACCGCTAAACAATATACCGTTCCTTGTGTTAACA 767
QY      99 -----GlnSerLeuSerPhe 103
DB      768 AAGTAAGAAAGAGAAACAATAACTTTGATTTGTTTATGTGTGACAGAGTTTGAAG 827
QY      103 GlySerValHisIleLeuSerGlyLeuLeuPheValLeuAlaTrpProIle----- 120
DB      828 AAGGCTTGTCATATCTCAGGTCTGCTTTTCGTAATCTGGGTGCGCAATCTTCAGGTA 887
QY      120 ----- 120

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DB      888 TTGCTTTCTCTATGATGTTGMAATCTCTGTGATCCTTTTAAACATGATAGATTCTGA 947
QY      121 -----PheSerGlySerThrGlnAlaArgTyraPheAlaAlaPh 133
DB      948 TTTCTTTTACTCATCTTTTAAGTTTAAGGATTCACCGAGCTCGATCTTGTGCTGCTT 1007
QY      133 eValProLeuValAsnGlyLeuArgLeuValIleAsnGlyLeuSerIleSerProAsnSe 153
DB      1008 TGTTCCTGATGATGAGCTTAAGCTGTGTATTAACGACTATCAATTTCCCAAAATTC 1067
QY      153 rMetLeuIleIysSerValThrArgGlnGlyArgAlaGlu----- 166
DB      1068 GATGCTATCAAAATCCGTCAACAGAGAAGGAGCAGAGTAAGTTGTCTAGTTTATTTT 1127
QY      166 ----- 166
DB      1128 TCCAACTTGATATGATTTTCAACAATCTGATTAACACATTTCTGTTTCCAAACATCA 1187
QY      167 ----GlnLeuLeuGlyGlyProLeuPheTyraValLeuAlaLeuLeuPheSerAlaValPh 185
DB      1188 CAGAGAGTTGCTTAAGGTCCTTGTCTAGCTCTAGCTCTCTCTTCTCTGCGGCTTTT 1247
QY      185 ePheTrpArgGlnSerProIleGlyMetIleSerLeuAlaMetMetCyArgIleArgGly 205
DB      1248 CTTCGAGAGAGTCTCTATCGGTATGATCTCGTTAGCAATGATGTGTGGGATGG 1307
QY      205 YIle----- 206
DB      1308 TAA-ATTTTCGTCAAGTACTGTATTAATTAATTAATTAATTAATTAATTAATTA 1366
QY      207 -----AlaAspIleMetGlyAr 212
DB      1367 ATGTACTAATAAGTGTGATCAATATGCTATGATGAGATAGCTGATTAATTAATTA 1426
QY      212 GlyPheGlySerThrTyraIleProTyraAsnProArgIleSerTrpAlaGlySerIleSe 232
DB      1427 TAAAGTTGGTCACTAAGATTAACCTTACCAACCAAGAAAGATTAAGGAGAGCATCTC 1486
QY      232 rMetPheIlePheGlyPhePheIleSerIleAla----- 243
DB      1487 CATGTTCACTTCGGCTTCTTCAATCTCATATCGC-GTAAATAATTAACCAATCCACTATT 1545
QY      243 ----- 243
DB      1546 AATCATCAAAATGTCTCCTCTGTGACGAAACAAGTCTTAAGAACTGAGTAGCTTGC 1605
QY      244 -----LeuLeuTyraTyraSerSerIle 251
DB      1606 TACTAACCCTAACCGTTTCTTTGTGAATTTTGCAGATTACTTATTAATCTCAAGCT 1665
QY      251 uGlyTyraLeuHisMetAsnTrpGluThrThrLeuGlnArgValAlaMetValSerMetVa 271
DB      1666 TGGTACTTTCATGAATGAACTGGAAACGACCTTGACAGAGATGACAAATGCTCAATGCT 1725
QY      271 lAlaThrValValGlnSerLeuProIleThrAspGlnLeuAspAsnIleSerValPr 291
DB      1726 CGCCACGGTAGTCCAGTGTGCTAACCCATCAACGATCAATTAAGACGCAATATTCGTTCC 1785
QY      291 cLeuAlaThrIleLeuAlaIleTyraLeuSerPheGlyTyra 304
DB      1786 TCTGGCTACTATTTTAACTGCTTATTTAAGTTTGGGATAT 1825

```

RESULT 5

US-10-425-114-29129
 ; Sequence 29129, Application US/10425114
 ; Publication No. US20040034688A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack B
 ; APPLICANT: Cao, Yongwei

```

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 29129
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB82-020-E9_FLI
US-10-425-114-29129

Alignment Scores:
Pred. No.: 2,366-144 Length: 1062
Score: 1266.00 Matches: 250
Percent Similarity: 89.3% Conservative: 24
Best Local Similarity: 81.4% Mismatches: 27
Query Match: 82.4% Indels: 6
DB: 7 Gaps: 2

US-10-634-548-2 (1-304) x US-10-425-114-29129 (1-1062)

QY 1 MetAlaAlaThrLeuProLeuSerProIlleAenHlsgInLeuCyArgPheGlyAenAen 20
Db 46 ATGGCGGAGCGCTTATCTTATCTCCGTTACCATCACTATATGTCGATAGCAACAG 105
QY 21 -----SerLeuThrThrlHlArgPheCySerProGlyPheLeuIlleSerPro 37
Db 106 TTCTGATTAACGCTATACCTCCCGGTTCTGTCGCA-----GTTCTTCGCC 156
QY 38 CysPheIlleGlyLeuThrGlyMetGlySerAlaThrInLeuArgAlaArgArserLeu 57
Db 157 TGTATCATCGCGGCTTAAAGAAATCGGCTCGTCAAGTATTAACGCGCTCGCACCCCTCG 216
QY 58 IlleSerSerAlaValAlaThrAenSerLeuLeuHlAenValGlyAlaThrValAlaVal 77
Db 217 ATCTCTTACGCGGCTTCACTATATCTATTCATGACATGAGCTGAGGCCACGCTGCAATT 276
QY 78 LeuGlyGlyAlaThrAlaLeuValLeuSerPheGlySerLeuThrLyArgAenValIlle 97
Db 277 CTATAGTGGAGCTTACGCGCTTGTCTTACTCTCGAAGATCTACAGAGGAGAGCTGAT 336
QY 98 GlngInserLeuSerArgLyLeuValHlAenLeuSerGlyLeuLeuPheValLeuAla 117
Db 337 CCACAGAGATTGACAGAAAGCTTGTGATATATCTCAAGTCTCTTTCGCGCTCG 396
QY 118 TrpProIllePheSerGlySerThrGluAlaArgTyrrPheAlaAlaPheValProLeuVal 137
Db 397 TGGCCATCTTCAGCGCATCAACGAGGCTCGATCTTGTCTGCTTGTTCCTTATAGTG 456
QY 138 AenGlyLeuArgLeuValIlleAenGlyLeuSerIlleSerProAenSerMetLeuIlleLys 157
Db 457 AATGGCCTTAAGGCTTGTGTCAACGCTTGTTCGCTCCCTCAATCCACGCTATTCOA 516
QY 158 SerValThrArgGlyArgAlaGluGluLeuLeuGlyGlyProLeuPheTyrrValLeu 177
Db 517 TCCGTAATCAGGAGAGAAACCAAGAGCTTGAAGGTCATTAAGGTCATTTGCTTACCTTCA 576
QY 178 AlaLeuLeuPheSerAlaValAlaPhePheTrpArgGlySerProIlleGlyMetIlleSerLeu 197
Db 577 GCCCTTCTTACGCTTCAAGCTTCTTCTGAGAGATCTTCTTCAACCGATATGATATCGCTG 636
QY 198 AlaMetMetCyGlyGlyAspGlyIleAlaAenIlleMetGlyArgLyArgPheGlySerThr 217
Db 637 GCAATGATGTGTGGCGACGGAATAGCTGATATCATGCGACGTAAGAACGATCATAC 696
QY 218 LysIlleProTyrrAenProArgLySerTrpAlaGlySerIlleSerMetPheIllePheGly 237
Db 697 AAGATTAACCTTACCAACCAAGAAAGCTTGGCGGAGAGATCTTCATATGTTATTCGCG 756
QY 238 PhePheIlleSerIlleAlaLeuLeuTyrrTyrrSerSerLeuGlyTyrrIlleHlMetAen 257

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Db 757 TTCTTATCTTCATCGATGATTAATCTTACTTATCTCAACGCTAGGATATCTTCACTGAC 816
QY 258 TrpGluThrThrLeuGluArgValAlaMetValSerMetValAlaThrValAlaGluSer 277
Db 817 TGGGAAACACACTTATACAGAGTCCGATTTGCTCATTTGATGTCGTAACGTGTGAGTCA 876
QY 278 LeuProIlleTrpAspGluLeuAenAenAenIlleSerValProLeuAlaThrIlleLeuAla 297
Db 877 CTACCATCAACCGATCAATATACAGCAACGTTTGGTTCTCTGCTACTATATTTGGCT 936
QY 298 AlaTyrrLeuSerPheGlyTyrr 304
Db 937 GCTTACCTTAAGTTTGGATAT 957

RESULT 6
US-10-425-114-20410
; Sequence 20410, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven B
; APPLICANT: Tabaska, Jack B
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 20410
; LENGTH: 1007
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3196-048-A11_FLI
US-10-425-114-20410

Alignment Scores:
Pred. No.: 8,196-96 Length: 1007
Score: 870.00 Matches: 174
Percent Similarity: 73.3% Conservative: 51
Best Local Similarity: 56.7% Mismatches: 72
Query Match: 56.6% Indels: 10
DB: 7 Gaps: 2

US-10-634-548-2 (1-304) x US-10-425-114-20410 (1-1007)

QY 2 AlaAlaThrLeuProLeuSerProIlleAenHlsgInLeuCyArgPheGlyAenAenSer 21
Db 18 GCTGTACCAAGAGGCTCTCC-----TTATCCTTCACTCATCAATC 59
QY 22 LeuThrThrlHlArgPheCySer-----ProGlyPheLeuIlleSerSerPro 37
Db 60 TTAAAGCCGCAAGCTATATCCGCGTATTTCTCTCCCTCCGTTTCTCTCTCTCTCT 119
QY 38 CysPheIlleGlyLeuThrGlyMetGlySerAlaThrGluLeuArgAlaArgArserLeu 57
Db 120 CTCATCCCAACAGATCCGTTTCCCTATTTCTACACGCGGCCCAAGCGCACCGCA 179
QY 58 IlleSerSerAlaValAlaThrAenSerLeuLeuHlAenValGlyAlaThrValAlaVal 77
Db 180 CTCTCAGCAACCGCTGTAACCGCTCTATCTTCGAGATACCGGCTGCTTCCGCTCTGTC 239
QY 78 LeuGlyGlyAlaThrAlaLeuValLeuSerPheGlySerLeuThrLyArgAenValIlle 97
Db 240 TTTCGTGCGCTTATGCTCTGCTCTTCACTTCACTTCTCACTCAAAAGAGCTATT 299
QY 98 GlngInserLeuSerArgLyLeuValHlAenLeuSerGlyLeuLeuPheValLeuAla 117
Db 300 CAGCAGATTTAAGTAAGAAATGCTGTGCAATATATCTGATTAATCTTTGCACTTTC 359

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Db 1645 CCGGCGGTCGCGCGCTCGGCGAGCGCCGCGCGCTCGGCGAGTCCGCC 1704
 QY 74 ThrValAlaValLeuGlyGlyValAlaLeuValLeuSerPheGluSerLeuThrLys 93
 Db 1705 ACGGTCGTCATCACCGCGCGCGCTGCTCCGCGCGCGCTGAGCGGCTCACCGCG 1764
 QY 94 ArgAenValIleGlnGlnSerLeuSerArgLysLeuValHisIleLeuSerGlyLeuLeu 113
 Db 1765 CCGCGGCTCATGACAGAACACTGAGCAGAAATTTGTCATGTCCTCCGGAATCCCG 1824
 QY 114 PheValIleuAlaATPProIlePheSerGlySerThrGlnAlaArgTyPheAlaAlaPhe 133
 Db 1825 TTCATGTCCTCCGCGCACTATTCAGTAATTCAGAACAGACCGGTCCTCCGCAAT 1884
 QY 134 ValProLeuValAlaGlyGlyLeuArgLeuValIleAenGlyLeuSerIleSerProAenSer 153
 Db 1885 GTCGCGGTCGTAACGCTAAGGCTTCGACCTACCGGCTCCGCTTCACATGAA 1944
 QY 154 MetLeuIleLysSerValThrArgGlnGlyArgAlaGlnGluLeuLeuLysGlyProLeu 173
 Db 1945 GCTCTAGTAATTCGCTGACCCGTAAGGAAACAGAGAAATTCGTAGAGCTCTCG 2004
 QY 174 PheTyValAlaLeuAlaLeuPheSerAlaValPhePheTrpArgGluSerProIleGly 193
 Db 2005 TACTATGTCATGTCGCTGCTGTCAGTGTTCGCTTCGCGCCAGCTCTCTATTTGG 2064
 QY 194 MetIleSerLeuAlaMetMetCysGlyGlyAspGlyIleAlaAspIleMetGlyArgLys 213
 Db 2065 ATGTGTTGCTGTTCATGTAAGAGTGAGTGAGGCTTTGCTGACATTTGAGAGAGAG 2124
 QY 214 PheGlySerThrLysIleProTyArgProArgLysSerTrpAlaGlySerIleSerMet 233
 Db 2125 TATGCTCCGCGAGAGCTGCTCATTCATAGAAACAGAGCTGATGGAAGCATTCATG 2184
 QY 234 PheIlePheGlyPhePheIleSerIleAlaLeuLeuTyTyTySerSerLeuGlyTyTy 253
 Db 2185 TTCATTTTCGCTCTCTCTATCTGACATGATGCTGCTCTCTCTCTCTCTCTCTCT 2244
 QY 254 LeuHisMetAenTrpGluThrThrLeuGlnArgValAlaMetValSerMetValAlaThr 273
 Db 2245 TTCACGTGTCGCGGATTCGCACTTGGAATCGGCTTGTCATTCATTCAGCACTACT 2304
 QY 274 ValValGluSerLeuProIleThrAspGlnLeuAspAspAsnIleSerValProLeuAla 293
 Db 2305 GTAGTGAGATGATTCCTCTCATATGATGTTGGAGAGACAAATATCTCGTTCTTGGCC 2364
 QY 294 ThrIleLeuAlaAlaTyLeuSerPheGlyTyTy 304
 Db 2365 ACCATGTTGCGAGCTATCTGTTATTTGGCTAC 2397
 RESULT 10
 US-10-425-114-26593
 / Sequence 26593, Application US/10425114
 / Publication No. US20040034888A1
 / GENERAL INFORMATION:
 / APPLICANT: Liu, Jindong
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Kovalic, David K.
 / APPLICANT: Screen, Steven E.
 / APPLICANT: Tabaka, Jack E.
 / APPLICANT: Cao, Yongwei
 / TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 / FILE REFERENCE: 38-21(5313)B
 / CURRENT APPLICATION NUMBER: US/10/425,114
 / NUMBER OF SEQ ID NOS: 71128
 / SEQ ID NO 26593
 / LENGTH: 1033
 / TYPE: DNA
 / ORGANISM: Oryza sativa
 / FEATURE:
 / OTHER INFORMATION: Clone ID: LIB4371-003-F9_FLI

US-10-425-114-26593
 Alignment Scores:
 Pred. No.: 9,78e-86 Length: 1033
 Score: 788.00 Matches: 160
 Percent Similarity: 71.2% Conservative: 60
 Best Local Similarity: 51.8% Mismatches: 76
 Query Match: 51.3% Indels: 13
 DB: 7 Gaps: 3
 US-10-634-548-2 (1-304) x US-10-425-114-26593 (1-1033)
 QY 6 ProLeuSerProIleAenHisGlnLeuCysArg-----PheGlyAsnAenSerLeu 22
 Db 6 CCGCGAGCGTCGCGCGCACTCCCGGCTCTCTGTCGTCGCGCGCTCTCTCTCTCT 65
 QY 23 -----ThrThiAenArgPheCysSerProGlyPheLeuIleSerSer-ProCys 38
 Db 66 CTGCTGCGCGCTCCAGTCCAGGCTCGGCTCTGCGCGCGCGCGCGAGCTTCATG 125
 QY 38 sPheIleGlyLeu--ThrGlyMetGlySerAlaThrGlnLeuArgAlaArgSerLeu 57
 Db 126 CCGCGAAGGCTTGTGCTCGCGGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 176
 QY 58 IleserSerAlaValAlaThrAenSerLeuLeuHisAenValGlyAlaThrValAlaVal 77
 Db 177 GCGCTGCGCGCTGCGCGAGCGCGCGCGCTGCGCGAGCTCGCGCGCACTGCTCATC 236
 QY 78 LeuGlyGlyAlaTyValAlaLeuValLeuSerPheGluSerLeuThrArgAenValIle 97
 Db 237 ACCGCGGCGGCTATCTCTGTCGCGCGCTTCGAGGCTTCACGCGCGCGCGCGCTATC 296
 QY 98 GlnGlnSerLeuSerArgLysLeuValHisIleLeuSerGlyLeuLeuPheValLeuAla 117
 Db 297 GACAGAGACCTGAGAGAAATTTGTCATGCTCTCGAGGCTCTGTCATGCTCTCC 356
 QY 118 TrpProIlePheSerGlySerThrGlnAlaArgTyTyPheAlaAlaPheValProLeuVal 137
 Db 357 TGGCCCATTCATCAGTAATTCACAGAACAGAGCTCTTCGCGCGCAATTTCTCCGTTGCTG 416
 QY 138 AenGlyLeuAlaGlyLeuValIleAenGlyLeuSerIleSerProAenSerMetLeuIleLys 157
 Db 417 AACGCAATAGGCTTCTACCTACCGAGCTCCGCTTCACATGAGAACTTATGTAANA 476
 QY 158 SerValThrArgGlnGlyArgAlaGlnGluLeuLeuLysGlyProLeuPheTyValLeu 177
 Db 477 TCGGAGACCCGTAAGGAAACAGAGAAATTCGTAAGAGTCCCTGATCATATGTCATT 536
 QY 178 AlaLeuLeuPheSerAlaValPhePheTrpArgGluSerProIleGlyMetIleSerLeu 197
 Db 537 GTGCTGTCGTCAGGTTTGTCTTCGCGCGCACTCTCCATATGGGATTTGTTGCTTG 596
 QY 198 AlaMetMetCysGlyGlyAspGlyIleAlaAspIleMetGlyArgLysPheGlySerThr 217
 Db 597 TCGATGATGAGTGTGAGTATGCTTGTGTCATTTGAGAGAGATATGATGCTCCGCG 656
 QY 218 LysIleProTyArgProArgLysSerTrpAlaGlySerIleSerMetPheIlePheGly 237
 Db 657 AAGCTGCCATTCATAGAACAGAGAGCTGAGTAAGAGATTCATATTCATTTCTGCG 716
 QY 238 PhePheIleSerIleAlaLeuLeuTyTyTyTySerSerLeuGlyTyTyLeuHisMetAen 257
 Db 717 TTCCTTATCTGACATGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 776
 QY 258 TrpGlnTrpThrLeuGlnArgValAlaMetValIleSerMetValAlaThrValAlaGluSer 277
 Db 777 TGGAGATCTGGCACTGTAACCTGCTCTGTCGCTTTCAGCTATTCATGAGAGTGT 836
 QY 278 LeuProIleThrAspGlnLeuAspAspAsnIleSerValProLeuAlaThrIleLeuAla 297
 Db 837 ATTCCTGTCATGATGATGTCGATGATGATATATCTCGTTCTTGGCCAGCATGTTGGCA 896
 QY 298 AlaTyLeuSerPheGlyTyTy 304


```

QY      140  LeuArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMetLeuIleYserVal 159
      241  ATGAGGCTTCTGATATATGAGACTCCGCTCTCACTGATGAGCTCTGTAAATCAATG 300
QY      160  ThrArgGluGlyArgAlaGluGluLeuLeuYserGlyProLeuPheTyValIleuAlaLeu 179
      301  ACAAGTGAAGGAAACAGAGGAAATTCCTGAGAGGTCCACTATTATGCTCGGTGCTG 360
QY      180  LeuPheSerAlaValPhePheTTPArgGluSerProIleGlyMetIleSerLeuAlaMet 199
      361  CTGTTCAGGGTTTATGCTCTTCGCGGTGAGTCCCATCGGAGATGCTCTTCCTGCAAG 420
QY      200  MetCysGlyGlyAspGlyIleAlaSerIleMetGlyArgLeuPheGlySerThrIleVal 219
      421  ATGACCGGTGCGCATGGTTTCTCTCACTATTTGGAGAGAGATAGGCTCAGCGAAGCTG 480
QY      220  ProTyrAsnProArgLeuSerTTPAlaGlySerIleSerMetPheIlePheGlyPhePhe 239
      481  CCATTCAATCGGAGAGAGAGCTGGGCGGAGCATCTGATGTTCAATTTCTGTTCCCTG 540
QY      240  IleSerIleAlaLeuLeuTyTyTyTySerSerLeuGlyTyLeuHiMetAsnTTPGlu 259
      541  CTGTCCGCGATGATGCTCTCACTTCACAGCTGGGTTACATGATGATTCCTGGAGA 600
QY      260  ThrThrLeuGlnArgValAlaMetValIleSerMetValAlaThrValAlaGluSerLeuPro 279
      601  GAGGACCTTGGTAAAGCTGCGCTGTTTGACATGACGACGACGATGAGTGGCTTCT 660
QY      280  IleThrAspGlnLeuAspAspAsnIleSerValProLeuAlaThrIleLeuAlaIleTy 299
      661  GAGACCGAAGTTGTGATGACAAATATCTGTTCTTGGCCACATGCTGTTAGCTTTT 720
QY      300  LeuSerPhe 302
      721  CTCTGTGTTT 729
DB

```

RESULT 13
US-10-425-114-26551
Sequence 26551, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425, 114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 26551
LENGTH: 976
TYPE: DNA
ORGANISM: Triticum aestivum
FEATURE:
OTHER INFORMATION: Clone ID: LIB4312-010-Cl1_FLI
US-10-425-114-26551

Alignment Scores:
Pred. No.: 6,17e-84 Length: 976
Score: 773.00 Matches: 149
Percent Similarity: 70.9% Conservative: 56
Best Local Similarity: 51.6% Mismatches: 66
Query Match: 50.3% Indels: 18
DB: 7 Gaps: 1

US-10-634-548-2 (1-304) x US-10-425-114-26551 (1-976)
QY 33 LeuIleSerSerProCysPheIleGlyLeuThrGlyMetGlySerAlaThrGlnLeuArg 52

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DB      60  CTCCTCTCTCCCGACCTGCTGCTGCGGCTTCACCTCCGCCCGGACCTCGCC 119
QY      53  AlaArgArg----- 55
DB      120  GCGCGAGGCGGAGCGGCTGCTGCGCGGCGCGGCGCGGCGCGGCGGCGGCGGCGGCGG 179
QY      56  ---SerLeuIleSerSerAlaValAlaThrAsnSerLeuLeuHiAspValGlyAlaThr 74
DB      180  CTGCGGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 239
QY      75  ValAlaValLeuGlyGlyAlaTyTyTyTyValLeuValLeuSerPheGluSerLeuThrIleArg 94
DB      240  CTGCTCGTCAACCGCGCGGCGCTACTCTCTCTGCGCGCGCTTCGACGCGCTCACCGAGGCG 299
QY      95  AsnValIleGlnIleSerLeuSerArgLeuValHisIleLeuSerGlyLeuLeuPhe 114
DB      300  CGCTCGTCAACAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 359
QY      115  ValLeuAlaTTPProIlePheSerGlySerThrGluAlaArgTyPheAlaAlaPheVal 134
DB      360  ATGGCTTCATGCGCATCTTTCAGCAATTCATCAAGTGACAGGTTCTTTCGACGCGGTAGT 419
QY      135  ProLeuValAsnGlyLeuArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMet 154
DB      420  CCGTTCCTGAACCTGCGTAAAGCTTCTCACTACGCGGCTCGCTTACTCCGACGAGACT 479
QY      155  LeuIleYserSerValIleThrArgGluGlyArgAlaGluGluLeuLeuYserGlyProLeuPhe 174
DB      480  CTAGTAATATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 539
QY      175  TyrValLeuAlaLeuLeuPheSerAlaValPhePheTTPArgGluSerProIleGlyMet 194
DB      540  TATGTCATCGTCACTGATCATTTGTTCTAGTCTTTTGGCGGAGCTCCCGCATCGGAGATC 599
QY      195  IleSerLeuAlaMetMetCysGlyGlyAspGlyIleAlaAspIleMetGlyArgYserPhe 214
DB      600  GTTTCCTGTCGATGATGAGCGGTGTCACGCTTTCGTCATTTGTCGAGAGAGAGGTC 659
QY      215  GlySerThrIlePheProTyrAsnProArgYserTTPAlaGlySerIleSerMetPhe 234
DB      660  GCTTCGTCAGAGCTGCCATTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
QY      235  IlePheGlyPhePheIleSerIleAlaLeuLeuTyTyTyTySerSerLeuGlyTyLeu 254
DB      720  ATCTCGGTTCCGCTATCTGCACTGATGCTGCTCTATTCCTGCTGCTGTTGTTATCATC 779
QY      255  HisMetAsnTTPGluThrThrLeuGlnArgValAlaMetValSerMetValAlaThrVal 274
DB      780  CATGTCACCTGGAGTACAGCGCTGTTGTAACCTGTTGCTGCTGCGCTGCGACGACCTG 839
QY      275  ValGluSerLeuProIleThrAspGlnLeuAspAsnIleSerValProLeuAlaThr 294
DB      840  GTGAGGTATTCCTGTAAGTATGTTGTAATGACATATCTCTGTTCCCTTGGCCAC 899
QY      295  IleLeuAlaAlaTyTyTyTyLeuSerPheGly 303
DB      900  ATGTTGTAGCTTCTCTGTTGTTGCG 926

```

RESULT 14
US-10-425-114-26571
Sequence 26571, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425, 114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 26571
LENGTH: 976
TYPE: DNA
ORGANISM: Triticum aestivum
FEATURE:
OTHER INFORMATION: Clone ID: LIB4312-010-Cl1_FLI
US-10-425-114-26571

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; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 25671
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB957-022-E3_PL1
US-10-425-114-25671

Alignment Scores:
Pred. No.: 1,9e-81      Length: 723
Score: 751.00      Matches: 137
Percent Similarity: 83.0%      Conservative: 48
Best Local Similarity: 61.4%      Mismatches: 38
Query Match: 48.9%      Indels: 0
DB: 7      Gaps: 0

US-10-634-548-2 (1-304) x US-10-425-114-25671 (1-723)

QY 80 GYALAATYRALeUValLeuSerPheGluSerLeuThrIlyarGhenValIleGlnGln 99
Db 7 GGCGGCTACTCTTGTGTGGCGGCTTCGACGAGCTCAACGAGCGGCGGCTCATCGAAG 66

QY 100 SerLeuSerArgIlyLeuValHisIleLeuSerGlyLeuLeuPheValLeuAATPPro 119
Db 67 AGCTTGAGCAGAGAGGTGTGACCGGTGCGGTGCGGCTCTGTTCAATGTCATCTGGCCC 126

QY 120 IlePheSerGlySerTherGluIlaaGTYrPheAlaIaPheValIProLeuValaangIly 139
Db 127 CTGTTCAAGCAATTCACAGAGACCGGATTTCCGCGGCTGTCCCTTCGAACTCC 186

QY 140 LeuArgLeuValIleangIlyLeuSerIleSerProaSerMetLeuIleIySerVal 159
Db 187 ATGAGGCTTCTGATATATGAGACTCGCTCTCACTAGATGAACTCTGTAATACATG 246

QY 160 ThrArgGluGlyAArgAlaGluGluLeuLeuIyGlyProLeuPheTYrValLeuAlaLeu 179
Db 247 ACACCTGAGAGAAACCAAGAGGATTCGAGAGGTCCACTCATTAATGCTCGTGC 306

QY 180 LeuPheSerAlaValPhePheTYrParGluSerProIleGlyMetIleSerLeuAlaMet 199
Db 307 CTGTTACAGGCTTTTACTCTTCTGGCGGTAGTCCCAATCGGAGATCGTCTCTGTGCATG 366

QY 200 MetCysGlyGlyAAspGlyIleAlaAspIleMetGlyAArgIyAPheGlySerThryIle 219
Db 367 ATGACCGGTGGCGATGGTTCCCTGACATTTGGGAGAGAGATATGGCTCAGCGAAGCTG 426

QY 220 ProTYraenProArgIySerTYrPalagIySerIleSerMetPheIlePheGlyPhePhe 239
Db 427 CCATTCAATCCGAGAGAGAGAGCTGGGCGCGGAGCATTCGATGTTCAATTTCTGGATTCCTG 486

QY 240 IleSerIleAlaLeuLeuTYrTYrTYrSerSerLeuGlyTYrIleuHisMetAenTPGlu 259
Db 487 CTGTCGCGCATGATGATGCTCATCTTCTCAAGCTTGGTTACATTAATGATTAATCTGGAA 546

QY 260 ThrThrLeuGlnAArgValAlaMetValISerMetValAlaThryValIaGluSerLeuPro 279
Db 547 GAGGCACTTGCTGATAGCTGGCGCTGTGTGCACTAGCAGCAGCACTAATGATGAGTGCCTTCT 606

QY 280 IleThrAPGlnLeuAAspAAspAnilIleSerValIProLeuAlaThrIleLeuAlaIlyr 299
Db 607 GTGACCGCAAGTGTATGATGACAATATCTGTTGCTTTGGCCACCATGCTGTAGCTTTT 666

QY 300 LeuSerPhe 302
Db 667 CTCTTGTTT 675

RESULT 15
US-10-425-114-26498
; Sequence 26498, Application US/10425114
; Publication No. US20040034888A1

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: GENERAL INFORMATION:
: APPLICANT: Liu, Jindong
: APPLICANT: Zhou, Yihua
: APPLICANT: Kowalic, David K.
: APPLICANT: Screen, Steven E
: APPLICANT: Tabaska, Jack E
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
: FILE REFERENCE: 38-21(5313)B
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 73128
: SEQ ID NO 26498
: LENGTH: 753
: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: OTHER INFORMATION: Clone ID: LIB4185-055-C9_FLI
US-10-425-114-26498

Alignment Scores:
Pred. No.: 2.03e-81 Length: 753
Score: 751.00 Matches: 137
Percent Similarity: 83.0% Conservative: 48
Best Local Similarity: 61.4% Mismatches: 38
Query Match: 48.9% Indels: 0
DB: Gaps: 0

US-10-634-548-2 (1-304) x US-10-425-114-26498 (1-753)

QY 80 GYALATYALALAEUVALLEUSERPHGLSEURTHLYRARGANVALLGGLNGIN 99
DB 16 GCGCGCTACTCTCTTGTCCGCGCTCTCACGAGCTCACCGAGCGCGCTCATCGAAG 75
QY 100 SERUSEARGLYBLAEUVAHISITLEUSERGILYLEUPEHAEUVALLEUATTPRO 119
DB 76 AGCTTGACAGAGAGAGTGTGACGTGCTGCGCGCTGTCTATGATGATCTTGCGCC 135
QY 120 LLEPHESERGIYSETHRIGUALAARGTYRPHAAALAPHEVALPROLEUVALANGY 139
DB 136 CTGTTTCAGCAATTGCACAGAGACACGATATTTCCGCGCGGTGTCCCGTTCGAATCC 195
QY 140 LEUARGLEUVALLEANGYLYSEURILESERPROANSEMERLEUILLYSEURVAL 159
DB 196 ATGAGGCTTCGATATATGAGACTCCGCTCTACACTGATGAGACCTCTGTAATAATCAGTG 255
QY 160 THRARGIGUGLYARGALAGLUGLNULEUYSGLYPROLEUPHETRYVALLEUVALLEU 179
DB 256 ACAGGTGAGAGAAAACGAGAGAAATGTGAGAGGTCCACTATATATCTCTGCGTGCG 315
QY 180 LEUPHESERIALAVALPHEPHETRYARGLUSERPROILEGLYMETILESERLEUAMET 199
DB 316 CTGTTTCAGCGTTTATGATCTTCTGCGGTAGTCCGCCATCCGGATGCTCTCTGTGCGAG 375
QY 200 MECYSGIYGLYAPSGYLYLEALAPLLEMETGLYARGLYSPHEGLYSETHRYLSTIE 219
DB 376 ATGAGCGGTGCGATGATGTTGCTGCTGACATYGTGGGAGAGAGTATGAGCTCACGGAAGCTG 435
QY 220 PROTRYANPROAGLYSESTTRPALAALYSERIIESERMEPHILPEHELYPHEPHE 239
DB 436 CCATTCAATCGAAGAGACGCTGGCGCGGAGACATCGATGTTCAATTCGTGTTTCCG 495
QY 240 LLESERILEALALEUETRYTYRSESERLEUGLYTYRLEUHIAMETANTRPGIU 259
DB 496 CTGTCCCGGAGATGATGATCTCTACTCTTCACAGCCGCGGTATCATGATGATATCGGGA 555
QY 260 THRTHREUGINARGVALAMETVALSERMECVALLATIRVALVALGUSERLEUPRO 279
DB 556 GAGCAGCATGTTGAAGCTGCGCTTGTTCGACTAGACGAGACAGTATGATGAGCGCTTCT 615
QY 280 ILEHRAPGILNULEUAPAPANTLESERVALPROLEUALATHRIILEUVALALATYR 299
DB 615

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Db	616	GTGACCGAAGTTGTAGATGACAATATCTTCTTCTTGCCACCATGCTGTAGCTTTT	675
Qy	300	LeuSerPhe	302
Db	676	CTCTTGTTT	684

Search completed: March 16, 2006, 23:49:59
Job time : 915 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: March 16, 2006, 23:48:07 ; Search time 429 Seconds

(without alignments)
1652.304 Million cell updates/sec

Title: US-10-634-548-2

Perfect score: 1536

Sequence: 1 MAATLPSPINHQLCRFGNN.....DDNISVPLATIAATLSFGY 304

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+.p2n.model -DEV=xlh
-Q=/abs/ABSSWB.epool/US10634548/runat_16032006_084442_10504/app.query.fasta.1
-DB=Published Applications NA New -QFMT=fasta -SUFIX=p2n.rnpba -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Dlosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pcr -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcr -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abss02h
-USER=US10634548 @CGN 1 1 431 @runat_16032006_084442_10504 -NCPU=6 -ICPU=3
-NO MAP -NGS SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA New:*

1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	777.5	50.6	1198	US-11-096-568A-19558	Sequence 19558, A
2	613	39.9	986	US-11-096-568A-1769	Sequence 1769, A
3	562.5	36.6	1048	US-11-096-568A-14811	Sequence 14811, A
4	475	30.9	481	US-11-096-568A-14317	Sequence 14317, A

5	152.5	9.9	978	US-10-932-182A-81375	Sequence 81375, A
6	152.5	9.9	978	US-10-932-182A-81375	Sequence 81375, A
7	150	9.8	525	US-10-932-182A-174337	Sequence 174337, A
8	150	9.8	525	US-10-932-182A-174337	Sequence 174337, A
9	143.5	9.3	804	US-10-932-182A-80837	Sequence 80837, A
10	143.5	9.3	804	US-10-932-182A-80837	Sequence 80837, A
11	143.5	9.3	1560	US-10-932-182A-1952	Sequence 1952, A
12	143.5	9.3	1560	US-10-932-182A-1952	Sequence 1952, A
13	115.5	7.5	7974	US-10-499-290-1	Sequence 1, Appl1
14	98.5	6.4	1152	US-10-793-626-2167	Sequence 2167, Ap
15	98.5	6.4	3108	US-10-793-626-3427	Sequence 3427, Ap
16	97	6.3	1296	US-11-092-140-5	Sequence 5, Appl1
17	97	6.3	2694	US-10-932-182A-78840	Sequence 78840, A
18	97	6.3	2694	US-10-932-182A-78840	Sequence 78840, A
19	95.5	6.2	867	US-11-194-246-495	Sequence 495, App
20	95.5	6.2	2037	US-11-096-568A-22288	Sequence 22288, A
21	95.5	6.2	2640	US-11-194-246-385	Sequence 385, App
22	95.5	6.2	2720	US-11-194-246-124	Sequence 124, App
23	95.5	6.2	8833	US-10-876-787-5	Sequence 5, Appl1
24	94.5	6.2	2085	US-10-485-517-391	Sequence 391, App
25	94.5	6.2	3840	US-10-793-626-4013	Sequence 4013, Ap
26	94.5	6.2	4235	US-10-793-626-4041	Sequence 4041, Ap
27	93.5	6.1	1230	US-10-793-626-2001	Sequence 2001, Ap
28	93.5	6.1	1230	US-10-793-626-2205	Sequence 2205, Ap
29	92.5	6.0	5121	US-11-052-554A-559	Sequence 559, App
30	91.5	6.0	1784	US-11-096-568A-23660	Sequence 23660, A
31	90.5	5.9	962	US-10-793-626-4349	Sequence 4349, Ap
32	90.5	5.9	1180	US-10-793-626-4391	Sequence 4391, Ap
33	90	5.9	1006	US-11-096-568A-33230	Sequence 33230, A
34	89	5.8	1482	US-10-467-657-4375	Sequence 4375, Ap
35	87.5	5.7	630	US-09-925-065A-61537	Sequence 61537, A
36	87.5	5.7	1345	US-11-000-463-474	Sequence 474, App
37	87.5	5.7	1842	US-10-932-182A-76836	Sequence 76836, A
38	87.5	5.7	1842	US-10-932-182A-76836	Sequence 76836, A
39	87.5	5.7	1992	US-11-000-463-2	Sequence 2, Appl1
40	87.5	5.7	2928	US-11-103-957-48	Sequence 48, Appl1
41	87	5.7	1539	US-11-087-099-23	Sequence 23, Appl1
42	87	5.7	2076	US-11-098-686-9401	Sequence 9401, Ap
43	87	5.7	3117	US-10-793-626-4005	Sequence 4005, Ap
44	87	5.7	1457619	US-11-098-686-87739	Sequence 8739, Ap
45	86.5	5.6	663	US-10-821-234-648	Sequence 648, App

ALIGNMENTS

RESULT 1
US-11-096-568A-19558
; Sequence 19558, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Theyxy
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; NUMBER OF SEQ ID NOS: 2005-04-01
; SEQ ID NO 19558
; LENGTH: 1198
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1198)
; OTHER INFORMATION: Ceres Seq. ID no. 12373616
US-11-096-568A-19558

Alignment Scores:
Pred. No.: 2,41e-72
Score: 777.50
Percent Similarity: 68.9%
Best Local Similarity: 50.2%
Query Match: 50.6%
Length: 1198
Matches: 155
Conservative: 58
Mismatches: 71
Indels: 25

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DB:          9          Gaps:          4
US-10-634-548-2 (1-304) x US-11-096-568A-19558 (1-1198)
QY          18 GlyAenAenSerLeuThrThriAaRphe-----
DB          176 GGTGGAAATCGCAGATTCCTCGCTGCTACCGGCACATGCTGCAGCGCGCGCTGG 235
QY          28 -----CySerProGlyPheLeuLeu-----SerSerProCyPheLeuLeu 42
DB          236 ACCGCGCGCGCAGTCCCGCAACTCGCTGCTGCTGCGCGCTGCTGCGCGCGCGCG 295
QY          43 ThrGlyMetGlySerAlaThrGlnLeuArgAlaArgSerLeuLeuSer----- 59
DB          296 CTCGCGCGCTTCCCGCGGAAGCTCCATCGG---AGCGCGCTCTCTCGCGCGCGCGCAC 352
QY          60 -----SerAlaValAlaThrAenSerLeuLeuAaPValGlyAla 73
DB          353 CCGCGCGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCTGCTGCGAGACGAGCGGCTC 412
QY          74 ThrValAlaValLeuGlyGlyAlaValAlaValLeuSerPheGlySerLeuThrLys 93
DB          413 ACTGTCCTCATCACCGCGCGCGCTTACTCTTGTGCGCGCTTGCAGCAGCTCACCGAG 472
QY          94 ArgAenValIleGlnGlnSerLeuSerArgLysLeuValIleIleLeuSerGlyLeuLeu 113
DB          473 CCGCGCGCTCATGAAAGAGCTTGAAGCAGAAAGTTGTGCACTGCTATCCGCGCTGCTG 532
QY          114 PheValLeuAlaValProIlePheSerGlySerThrGlnAlaArgTyrPheAlaAlaPhe 133
DB          533 TTCATGTCATCTTGGCCCTGTTGACAGCATTCGACAGAGACAGCGGATTTCCCGCGGCT 592
QY          134 ValProLeuValAaenGlyLeuArgLeuValIleAaenGlyLeuSerIleSerProAaenSer 153
DB          593 GTCGCCCTTCTGAACTCCATGAGGCTTGTGATATATGACTCGTCTTCACTGATGA 652
QY          154 MetLeuIleLeuSerValThrArgGlnGlyArgAlaGlnGlyLeuLeuSerGlyProLeu 173
DB          653 GCTCTGCTGAATCACTGACACGTGAAGAGAAACCGAGGAATGCTGAGAGGTCCATC 712
QY          174 PheTyrValLeuAlaLeuLeuPheSerAlaValPhePheTyrArgGlnSerProIleGly 193
DB          713 TATTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 772
QY          194 MetIleSerLeuAlaMetMetCysGlyGlyAaenGlyIleAlaAaenIleMetGlyArgLys 213
DB          773 ATCTGCTCTTGTGATGATGAGCGGCTGATGATGATGATGATGATGATGATGATG 832
QY          214 PheGlySerThrLysIleProTyrAaenProArgLysSerTyrAlaGlySerIleSerMet 233
DB          833 TATGCTTCAAGCAGAGCTGCTCATTCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 892
QY          234 PheIlePheGlyPhePheIleSerIleAlaLeuLeuTyrTyrTyrSerSerLeuGlyTyr 253
DB          893 TTCAATTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 952
QY          254 LeuHISerMetAaenTyrGlnThrThrLeuGlnArgValAlaMetValSerMetValAlaThr 273
DB          953 ATTGATGTTATCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1012
QY          274 ValValGlnSerLeuProIleThrAaenGlnLeuAaenAaenIleSerValProLeuAla 293
DB          1013 GTAGTGAAGGCTTCTCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1072
QY          294 ThrIleLeuAlaAlaTyrLeuSerPhe 302
DB          1073 ACCATGCTGGTACCTTTCTCTGTTT 1099

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; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 1769
; LENGTH: 986
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(986)
; OTHER INFORMATION: Ceres Seq. ID no. 15178973
US-11-096-568A-1769

Alignment Scores:
Pred. No.: 5,486-55 Length: 986
Score: 613.00 Matches: 125
Percent Similarity: 61.4% Conservative: 50
Best Local Similarity: 43.9% Mismatches: 54
Query Match: 39.9% Indels: 56
Gaps: 4

US-10-634-548-2 (1-304) x US-11-096-568A-1769 (1-986)
QY          29 SerProGlyPheLeuLeu-----SerSerProCyPheIleGlyLeuThrGlyMetGly 46
DB          68 TCCCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 127
QY          47 SerAlaThrGlnLeuArgAlaArgSerLeuIleSer----- 59
DB          128 CCGGAGGAGCTCATGCGG---AGCGGCTGCTGCTGCGGCTGCGGACACCCCGCGCGCGG 184
QY          60 -----SerAlaValAlaThrAaenSerLeuLeuHISaPValGlyAlaThrValAlaVal 77
DB          185 GCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCTGTCAGACGCGGCGGCTCATGCTCATC 244
QY          78 LeuGlyGlyAlaTyrAlaLeuValLeuSerPheGlnSerLeuThrLysArgAaenValIle 97
DB          245 ACCGCGCGGCTTACTTCTTGTGCGCGCTTGTGACAGAGCTTCAAGAGAGAGAGAGAG 304
QY          98 GlnGlnSerLeuSerArgLysLeuValIleAaenSerGlyLeuLeuPheValLeuAla 117
DB          305 GAAAGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 364
QY          118 TyrProIlePheSerGlySerThrGlnAlaArgTyrPheAlaAlaPheValProLeuVal 137
DB          365 TCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 376
QY          138 AaenGlyLeuArgLeuValIleAaenGlyLeuSerIleSerProAaenSerMetLeuIleLys 157
DB          376 ----- 376
QY          158 SerValThrArgGlnGlyArgAlaGlnGlyLeuLeuSerGlyProLeuPheTyrValLeu 177
DB          377 -----AGGGAATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 412
QY          178 AlaLeuLeuPheSerAlaValPhePheTyrArgGlnSerProIleGlyMetIleSerLeu 197
DB          413 GTGCTGCTGTTGAGCGCTTATGCTTCTGCGCTGAGTCCCGCATCCGGAATCGTCTCTG 472
QY          198 AlaMetMetCysGlyGlyAaenGlyIleAlaAaenIleMetGlyArgLysPheGlySerThr 217
DB          473 TCGATGATAGAGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 532
QY          218 LysIleProTyrAaenProArgLysSerTyrAlaGlySerIleSerMetPheIlePheGly 237
DB          533 AAGCTGCATTCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 592
QY          238 PhePheIleSerIleAlaLeuLeuTyrTyrTyrSerSerLeuGlyTyrLeuHISerMetAaen 257

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RESULT 2
 US-11-096-568A-1769
 ; Sequence 1769, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:

Db 593 TTCCTGCTGCCGATGATGCTTCTCAAGCCGCTTACATGATGTTATC 652
Qy 258 TTPGUTThrLeuGlnArgValAlaMetValSerMetValAlaThrValAlaGluSer 277
Db 653 TGGGAAGGACCTGTGTAAGCTGGCGCTGTGCACTGACGACGACATGATGAGTGC 712
Qy 278 LeuProIleThrAspGlnLeuAspAsnIleSerValProLeuAlaThrIleLeuAla 297
Db 713 GTTCTGTGACCGAAGCTTATGATGACATATCTGTTCTTGGCCACCATGCTGGTA 772
Qy 298 AlaTyrLeuSerPhe 302
Db 773 GCTTCTCTTCTT 787

RESULT 3
US-11-096-568A-14811
; Sequence 14811, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Theory
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 14811
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1048)
; OTHER INFORMATION: Ceres Seq. ID no. 1233653
US-11-096-568A-14811

Alignment Scores:
Pred. No.: 1,366-49 Length: 1048
Score: 562.50 Matches: 115
Percent Similarity: 60.4% Conservative: 53
Best Local Similarity: 41.4% Mismatches: 101
Query Match: 36.6% Indels: 9
DB: 9 Gaps: 4

US-10-634-548-2 (1-304) x US-11-096-568A-14811 (1-1048)
Qy 28 CysSerProGlyPheLeuIleSerSerProCysPheIleGlyLeuThrGlyMetGlySer 47
Db 92 TGTGGCGCT-----CGCTCAGCTCTTCCGCGCGCGCGACGACGTGCTTC 139
Qy 48 AlaThrGlnLeuArgAlaArgArgSerLeuIleSerSerAlaVal-----AlaThr 64
Db 140 GCAAGCGAG--CGACCCGAGGAGGCTACATGACGAGCGGCAATCTCGCTGAGGCGCGC 196
Qy 65 AsnSerLeuLeuHisAspValGlyValaThrValAlaValIleGlyValaTyrAlaLeu 84
Db 197 GGGGCGCTGGCCCACTGACCTAGAGTCTGACGTCTGACAGCGTGGTCCCTCCGCGCTC 256
Qy 85 ValLeuSerPheGluSerLeuThrIlyAspAsnValIleGlnGlnSerLeuSerArgIys 104
Db 257 CTCMAATCTTTGAGAGAGCTCGCAAGCGCGCGCTTCAGACAGAACTCAGCAGGAAG 316
Qy 105 LeuValHisIleLeuSerGlyLeuLeuPheValIleAlaTyrProIlePheSerGlySer 124
Db 317 CTTGTTCAATATMAAGCTGGGCTGGATTCATGCTCTTTGGCTCTTTTAAAGCTCTGA 376
Qy 125 ThrGlnAlaArgTyrPheAlaAlaPheValProLeuValAsnGlyLeuArgPheValIle 144
Db 377 TGGTATACCTCTTCTGCTGCGCTGACGACAGGGGTTAATTAATTAAGATGCTTCTTA 436
Qy 145 AsnGlyLeuSerIleSerProAsnSerMetLeuIleIysSerValThrArgGlnGlyArg 164
Db 437 CTGGGGCTGGGACTTATGAAAAGAGGCTATGTTAATCAATGAGCGCGCTCTGAGAT 496

Qy 165 AlaGlnLeuLeuIysGlyProLeuPheTyrValLeuAlaLeuLeuPheSerAlaVal 184
Db 497 TACAGGAACTTCTAAGAGGCCACATGATATGCTGCTACTATGACTTTGCAAGCTCT 556
Qy 185 PhePheTyrArgGluSerProIleGlyMetIleSerLeuAlaMetMetCysGlyIysAsp 204
Db 557 CTTTATGAGAACTCACTCACTGCTTATGACCTTATGACAACTTATGCTGCGGAT 616
Qy 205 GlyIleAlaAspIleMetGlyArgGlyPheGlySerThrIlyGlyLeuProTyrAsnProArg 224
Db 617 GGTATAGCCGATGTTGAGAGAGCGCTAGGTAAGAAAGCTTCATACATCCCAAC 676
Qy 225 LysSerTPAlaGlySerIleSerMetPheIlePheGlyPhePheIleSerIleAlaLeu 244
Db 677 AATCATATGCTGGAAGCATACAAATGAGCGGCTGTTCTTCCGCTCACTGAGGAT 736
Qy 245 LeuTyrTyrTyrSerSerLeuGlyTyrLeuHisMetAsnTyrGluThrThrLeuGlnArg 264
Db 737 ATGCAATCTTCCACACTTTCGCTTTATGAGAAACATGATGATGCTTTAAGC--- 793
Qy 265 ValAlaMetValSerMetValaThrValAlaGluSerLeuProIleThrAspGlnLeu 284
Db 794 TTCCTGCTGCTCTGTAGCTGACGACCTGTTGAATGCGACCCCATGACAGCAAGACTT 853
Qy 285 AspAspAsnIleSerValProLeuAlaThrIleLeuAlaAlaTyrLeuSerPhe 302
Db 854 GATGCAATTTGACTGTCTTTTGAATCATCTTCAATGTTGAGCTCATCTTT 907

RESULT 4
US-11-096-568A-14317
; Sequence 14317, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Theory
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 14317
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(481)
; OTHER INFORMATION: Ceres Seq. ID no. 3626194
US-11-096-568A-14317

Alignment Scores:
Pred. No.: 9,796-41 Length: 481
Score: 475.00 Matches: 85
Percent Similarity: 83.8% Conservative: 29
Best Local Similarity: 62.5% Mismatches: 22
Query Match: 30.9% Indels: 0
DB: 9 Gaps: 0

US-10-634-548-2 (1-304) x US-11-096-568A-14317 (1-481)
Qy 167 GluLeuLeuIysGlyProLeuPheTyrValLeuAlaLeuLeuPheSerAlaValPhePhe 186
Db 26 GAATTCGAGAGAGCTCACTATATATCTCGTGTGCTGCTTCAAGCGTTTAACTCTTC 85
Qy 187 TTPArgGluSerProIleGlyMetIleSerLeuAlaMetMetCysGlyIysAspGlyIle 206
Db 86 TGGCTGATGCTCCCATGAGATGCTCTCTTTCGATGATGAGAGCGTGGGATGTTT 145
Qy 207 AlaAspIleMetGlyArgGlyPheGlySerThrIlyGlyLeuProTyrAsnProArgIysSer 226
Db 146 GCTGCAATTTGTTGGAGAGGATATGCTCAAGCAAGCTGCATTCATCGAAGAGAGAGC 205

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Oy 227 TrpAlaGlySerIleSerMetPheIlePheGlyPhePheIleSerIleAlaLeuLeuYr 246
Db 206 TGGGCGGAGACATTCATTCATTTCTGTTCCGCTCTCCGCGATATGATGCTC 265
Oy 247 TTTTYSerSerLeuGlyTYrIleuHiSmeAenTPGIurThrThrLeuGlnArgValAla 266
Db 266 TACTCTCAAGCGCTGGGTACATGATGTATCTGGGAAGGCACTTGATGTAAGCTGCG 325
Oy 267 MetValSerMetValAlaThrValValGluSerLeuProIleThrAspGlnLeuAspAsp 286
Db 326 CTTGTGACCTGACGACACAGTACGTGAGTGGCTTCCTGTAACCGAAGTTGATGAC 385
Oy 287 AsnIleSerValProLeuAlaThrIleLeuAlaAlaTYrLeuSerPhe 302
Db 386 AACATATCTGTTCTTGGCCACATGCTGTGACTTTCTTGTGTT 433

RESULT 5
US-10-932-182A-81375
; Sequence 81375, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81375
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-81375

Alignment Scores:
Pred. No.: 4,23e-06 Length: 978
Score: 152.50 Matches: 59
Percent Similarity: 43.0% Conservative: 40
Best Local Similarity: 25.7% Mismatches: 84
Query Match: 9.9% Indels: 47
DB: 7 Gaps: 8

US-10-634-548-2 (1-304) x US-10-932-182A-81375 (1-978)
Oy 80 G1AATATYrAlaLeuValLeuSerPheGluSerLeuThrLYsArgAsnValIleGlnIn 99
Db 355 GCGCTTATTACTTTGACTGTATACGCGAGATTAATAAATAATGTTTATGCGCT 414
Oy 100 SerLeuSerArgLYsLeuValHisIleLeuSerGlyLeuLeuPheValLeuAlaTrpPro 119
Db 415 TTGATATACGCGCTTCATCATATTGTTATTGATCTGATA---AGACTTAACGCGCC 471
Oy 120 IlePheSerGlySerThrGlnAlaArgYrPheAlaAlaPheValProLeuValAsnGly 139
Db 472 TTTTTC----- 477
Oy 140 LeuArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMetLeuIleYSerVal 159
Db 478 -----AATATGCTTACTGTGAAGTGTG 501
Oy 160 ThrArgGluGlyArgAlaGluGluLeu-----LeuLYsGlyProLeuPheTYrValLeu 177
Db 502 GGTGGCGCTAATGAGAAAAGAGATTTCATACATACAAATGAGGATGTGATGTAACATCTT 561
Oy 178 AlaLeuLeuPheSerAlaValPhePheTrpArgGluSerProIleGlyMetIleSerLeu 197
Db 562 GGGTATATCTTTTCTTTTAACTTTTCTCTTAAGAT-----GTTACCTTAATATGCTTA 615
Oy 198 AlaMetMetCysGlyGlyAspGlyIleAlaAspIleMetClyArgLYsPheGlySerThr 217

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Db 616 TTTTGTCAAGTGTGTCGATACAGCGCCCAACTATTTGAGAAAGTATGTCATTTA 675
Oy 218 LysIleProTYrAsnProArgLYsSerTrpAlaGlySerIleSerMetPheIlePheGly 237
Db 676 ACACCCAAATTTGGCAGAAATAAATCCCTTCAGGTTGATAGCGGCTTACACTGTGT 735
Oy 238 PhePheIleSerIleAlaLeuLeuTYrTYrIleSerSerLeuGlyTYrIleuHiSmeAen 257
Db 736 ---GTTATCACCTGCTGCGTATTTTATGCGCATTTTGTCTGCTGCTACAGCTACAC 792
Oy 258 -----TTP-----GluThrIleLeuGlnArgValAlaMetValSer 269
Db 793 AACCTGGCAGATTCATATGAGCCAGAAACAGCAATTAAAGTTGAATATGCTATCC 852
Oy 270 MetValAlaThrValValGluSerLeuProIleThrAspGlnLeu-----AspAsp 286
Db 853 TTTTGGGTGCTGTGTAGTGTCTTGTAGTGAAGGTATAGATTGTTCAACTGGGATGAT 912
Oy 287 AsnIleSerValProLeuAlaThrIleLeu 296
Db 913 AATTCACTATTCCTGCTGTCATCACTT 942

RESULT 6
US-10-932-182A-81375
; Sequence 81375, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81375
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-81375

Alignment Scores:
Pred. No.: 4,23e-06 Length: 978
Score: 152.50 Matches: 59
Percent Similarity: 43.0% Conservative: 40
Best Local Similarity: 25.7% Mismatches: 84
Query Match: 9.9% Indels: 47
DB: 7 Gaps: 8

US-10-634-548-2 (1-304) x US-10-932-182A-81375 (1-978)
Oy 80 G1AATATYrAlaLeuValLeuSerPheGluSerLeuThrLYsArgAsnValIleGlnIn 99
Db 355 GCGCTTATTACTTTGACTGTATACGCGAGATTAATAAATAATGTTTATGCGCT 414
Oy 100 SerLeuSerArgLYsLeuValHisIleLeuSerGlyLeuLeuPheValLeuAlaTrpPro 119
Db 415 TTGATATACGCGCTTCATCATATTGTTATTGATCTGATA---AGACTTAACGCGCC 471
Oy 120 IlePheSerGlySerThrGlnAlaArgYrPheAlaAlaPheValProLeuValAsnGly 139
Db 472 TTTTTC----- 477
Oy 140 LeuArgLeuValIleAsnGlyLeuSerIleSerProAsnSerMetLeuIleYSerVal 159
Db 478 -----AATATGCTTACTGTGAAGTGTG 501
Oy 160 ThrArgGluGlyArgAlaGluGluLeu-----LeuLYsGlyProLeuPheTYrValLeu 177

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Db      502 GGTGGCTAATGAGAAAAAGAGATTACATACATCAATGGGTATTGTGTACATTTCT 561
Qy      178 AAlaLeuPheSerAlaValaPhePheTpaArgGluSerProIleGlyMetIleSerLeu 197
      552 GGGTAACTCTTCTTTTAACTTTTCTCTTAAAGAT-----GTTACCTTAATATCGTTA 615
Qy      198 AlaMetCysGlyGlyAspGlyIleAlaAspIleMetGlyArgGlyPheGlySerThr 217
      616 TTTTTCCTAAGTGGTCCGATACAGCCGCCGCAACATTGGAAGAAAGATGTCATTTA 675
Db      218 LysIleProTyrAsnProArgLysSerThrPalagIleSerIleSerMetPheIlePheGly 237
      676 ACAACCAATTGCGAAGAAATTAATCCCTTCAGAGTTGATAGTCGCGCTTACAGTTGT 735
Qy      238 PhePheIleSerIleAlaLeuLeuTyrTyrTyrSerSerLeuGlyTyrLeuHisMetLeu 257
      736 ---GTTATCACTGCTGGTATTATTAATGCTATTGTTCTGCTCCTACAGCATCGTCAAC 792
Qy      258 -----Trp-----GluThrThrLeuGlnArgValaAlaMetValSer 269
      793 AAACCTGGCAGATCCATCGACGAGCCGAGAAACAGACAGTTAAGTTGATATGCTATCC 852
Qy      270 MetValaIaThrValaGluSerLeuProIleThrAspGlnLeu-----AspAsp 286
      853 TTGTAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 912
Db      287 AsnIleSerValProLeuAlaThrIleLeu 296
      913 AATTCACTATTCTGCTCTGTCATCACTT 942

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RESULT 7
US-10-932-182A-174337
; Sequence 174337, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174337
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-174337

```

```

Alignment Scores:
Pred. No.: 3,51e-06 Length: 525
Score: 150.00 Matches: 52
Percent Similarity: 42.64 Conservative: 31
Best Local Similarity: 26.78 Mismatches: 64
Query Match: 9.8% Indels: 48
DB: Gaps: 6

```

```

US-10-634-548-2 (1-304) x US-10-932-182A-174337 (1-525)
Qy      116 LeuAlaTppProIlePheSerGlySerThrGlnAlaArgTyrPheAlaAlaPheValPro 135
      10 TTAACCTGCGCCCTTTTTC----- 27
Db      136 LeuValaGnglyLeuArgLeuValIleanglyLeuSerIleSerProAsnSerMetLeu 155
      28 -----AATATGCTTAT 39
Qy      156 IleYsSerValThrArgGnglyArgAlaGnglyLeu-----LeuYsGlyProLeu 173
      40 TGTAGCAGGTAGGTAGCTTATATGAGAAAAAGAGATTACACGTACACGCGGTATTG 99

```

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Qy      174 PheTyrValIleAlaLeuLeuPheSerAlaValaPhePheTpaArgGluSerProIleGly 193
      100 TGTAACTCTGCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 153
Qy      194 MetIleSerLeuAlaMetMetCysGlyGlyAspGlyIleAlaAspIleMetGlyArgGly 213
      154 TTGATATCATCTTCTCTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 213
Db      214 PheGlySerThrLysIleProTyrAsnProArgLysSerThrPalagIleSerIleSerMet 233
      214 TATGCTATTATTAACACCCAAATTGCGAGAAACAAATCTTTGCGAGCTCGATACCTGCA 273
Qy      234 Phe-----IlePheGlyPhePheIleSerIleAlaLeu 244
      274 TTACAGTTGGGGCATCAGTCTGTCACATTATTAATGTTATTTT-----ATACCACT 327
Qy      245 LeuTyrTyrTyrSerSerLeuGlyTyrLeuHisMetLeuThrThrThrLeuGlnArg 264
      328 TACTACTACGTCAATTAACCTGAGAGATGTAATGCACTCCGAGAAACAGTAATTAAGC 387
Db      265 ValaIaMetValSerMetValaIaThrValaGluSerLeuProIleThrAspGlnLeu 284
      388 TTGAATATGTTATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 447
Qy      285 -----AspAsnIleSerValProLeuAlaThrIleLeu 296
      448 TTCACTGGGAGTACACTTCATCTTCTGTCATCACTT 492

```

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RESULT 8
US-10-932-182A-174337
; Sequence 174337, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174337
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-174337

```

```

Alignment Scores:
Pred. No.: 3,51e-06 Length: 525
Score: 150.00 Matches: 52
Percent Similarity: 42.64 Conservative: 31
Best Local Similarity: 26.78 Mismatches: 64
Query Match: 9.8% Indels: 48
DB: Gaps: 6

```

```

US-10-634-548-2 (1-304) x US-10-932-182A-174337 (1-525)
Qy      116 LeuAlaTppProIlePheSerGlySerThrGlnAlaArgTyrPheAlaAlaPheValPro 135
      10 TTAACCTGCGCCCTTTTTC----- 27
Db      136 LeuValaGnglyLeuArgLeuValIleanglyLeuSerIleSerProAsnSerMetLeu 155
      28 -----AATATGCTTAT 39
Qy      156 IleYsSerValThrArgGnglyArgAlaGnglyLeu-----LeuYsGlyProLeu 173
      40 TGTAGCAGGTAGGTAGCTTATATGAGAAAAAGAGATTACACGTACACGCGGTATTG 99

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OY 174 PheTyrValLeuAlaLeuPheSerAlaValPhePheTrpArgGluSerProIleGly 193
DB 100 TGGTACCTCCCTGGGGGTGGTGTTCCTTGTATTTTTCCTCAAGAC-----GTTACT 153
OY 194 MetIleSerLeuAlaMetMetCysGlyGlyIleAlaSerIleMetGlyArgIlys 213
DB 154 TTGATATCATTTGTTCTACTAGTGTGTCGATACAGCCGCGACGATCGAAGGAAA 213
OY 214 PheGlySerThrLysIleProTyrAsnProArgIysSerTrpAlaGlySerIleSerMet 233
DB 214 TATGTCATTTTAAACCCAAATTGGCGAAGAACAAATCTCTGCGAGGCTCGATTACTCA 273
OY 234 Phe-----IlePheGlyPhePheIleSerIleAlaLeu 244
DB 274 TTACACGTTGGGGCCATCACTGTTGACATTTTATGTTATTTT-----ATACCAACT 327
OY 245 LeuTyrTyrSerSerLeuGlyTyrIleuHisMetAsnTrpGluThrThrLeuGlnArg 264
DB 328 TACTACTACGTCAATAAACCTGAGAGATTGAATGACATCCGAGAAACAAGTAATTAAAC 387
OY 265 ValAlaMetValSerMetValAlaThrValValIleGluSerLeuProIleThrAspGlnLeu 284
DB 388 TTGAATATGTTATCGTTGTAGTGTGTGTGCTGCAATTGAGCGAAAGTATTGATTTG 447
OY 285 -----AspAspAsnIleSerValProLeuAlaThrIleLeu 296
DB 448 TTCAACTGGAGTACCACTTCACTTCTCTGACTATCATCTCACTT 492

RESULT 9
US-10-932-182A-80837
; Sequence 80837, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80837
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-80837

Alignment Scores:
Pred. No.: 2,976-05 Length: 804
Score: 143.50 Matches: 57
Percent Similarity: 48.0% Conservative: 51
Best Local Similarity: 25.3% Mismatches: 74
Query Match: 9.3% Indels: 43
DB: 7 Gaps: 12

US-10-634-548-2 (1-304) x US-10-932-182A-80837 (1-804)
OY 84 LeuValIleuSerPheGluSer---LeuThrLysArgAsnValIleGlnGlnSerLeuSer 102
DB 169 CTTATACCTGCTCATACCAAGTATATTGATCGAAGACGTCATACGTTGAACACTCC 228
OY 103 ArgLysLeuValHisIleLeuSerGlyLeuLeuPheValIleuAlaTrpProIlePheSer 122
DB 229 CGAAATTTGGCATTTTC-----ATCATTTTCTTACTCATTAATACCGTCATTCOA 279
OY 123 GlySerThrGluAlaArgTyrPheAlaAlaPheValProLeuValIleGlnGlyLeuArgLeu 142
DB 280 ATGATATCA-----AACCTTTGGAAAAAT 303
OY 143 ValIleAsnGly-----LeuSerIleSerProAsnSerMetLeuIleLysSerVal 159

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DB 304 GCATTCGCCGAACAATACCACTCTCTTATCAATTGATACATTAAGATTTCAAACCTA 363
OY 160 ThrArgGluGlyArgAlaGluGluLeu----- 169
DB 364 CCGCGCTTAAAGATCTGCTATTTGAATTAACAATAAGAGTTTCTGATGATAGGACAC 423
OY 170 LysGlyProLeuPheTyr---ValLeuAlaLeuPhe-----SerAlaValPhePhe 186
DB 424 AGCGGCGCATTTGATCATATCATACCTTTATTTACTCTTCGAAATATCAACCTTTATTA 483
OY 187 TrpArgGluSerProIleGlyMetIleSerLeuAlaMetMetCysGlyGlyIle 206
DB 484 ATGAATAACTCTCCAAATCGGCTAATAGATTGGGAAT-----GGTGAATTCCTTA 534
OY 207 AlaAspIleMetGlyArgLysPheGlySerThrLysIleProTyrAsnProArgIysSer 226
DB 535 GCATCTATTATTGTGAAGAGTATGGCCGCACTTCCTTGAAA---GGTACACAAAACCT 591
OY 227 TrpAlaGlySerIleSerMetPheIlePheGlyPhePheIleSerIleAlaLeuLeuTyr 246
DB 592 TTAGAGGGAACCTTCGCTTATATAGTACAGATTATTCGTTGTTGATATTTGTTACGT 651
OY 247 TyrTyrSerSerLeuGlyTyrIleuHisMetAsnTrpGluThrThrLeuGlnArgValAla 266
DB 652 TTGTATTAAGCTGCAATTTTAAACCACTA-----ACTACTTTCAATGCTTACC 702
OY 267 MetValSerMetValAlaThrValValGluSerLeuProIleThrAspGlnLeuAspAsp 286
DB 703 CTTGTACACTG---AGTGAAGTGTCTAGAGGTATATAGTGTG-----CTTAATGAC 750
OY 287 AsnIleSerValPro 291
DB 751 AATATTGATATCACT 765

RESULT 10
US-10-932-182A-80837
; Sequence 80837, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80837
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-80837

Alignment Scores:
Pred. No.: 2,976-05 Length: 804
Score: 143.50 Matches: 57
Percent Similarity: 48.0% Conservative: 51
Best Local Similarity: 25.3% Mismatches: 74
Query Match: 9.3% Indels: 43
DB: 7 Gaps: 12

US-10-634-548-2 (1-304) x US-10-932-182A-80837 (1-804)
OY 84 LeuValIleuSerPheGluSer---LeuThrLysArgAsnValIleGlnGlnSerLeuSer 102
DB 169 CTTATACCTGCTCATACCAAGTATATTGATCGAAGACGTCATACGTTGAACACTCC 228
OY 103 ArgLysLeuValHisIleLeuSerGlyLeuLeuPheValIleuAlaTrpProIlePheSer 122

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Db      229 CGAANAATGGGATTTC-----ATCATTTTCTTACTCATATAACCGTATTCCAA 279
Qy      123 GlycerThrgluAlaArgTyrPheAlaAlaPheValProLeuValAsnGlyLeuArgLeu 142
Db      280 ATGGATTCA-----AACCTTGCGTGAATAAT 303
Qy      143 ValIleAsnGly-----LeuSerIleSerProAsnSerMetLeuIleLeuSerVal 159
Db      304 GCATTGCTCCGACAAATACACAGTCTTCTTATCAATAGTACATAGATTCAAAACCTTA 363
Qy      160 ThrArgGluGlyArgAlaGluGluLeu----- 169
Db      364 CCGCGCTTGAAGTCTATTGAATTAACAATAAGAGTTGCTGATGATAGGACCA 423
Qy      170 LysGlyProLeuPheTyr---ValLeuAlaLeuLeuPhe-----SerAlaValPhePhe 186
Db      424 AGCGGGCCATGATCATATCATACCTTATATTACCTTCGAAATCAACACCTTTATTA 483
Qy      187 TrpArgGluSerProIleGlyMetIleSerLeuAlaMetMetCysGlyValAspGlyIle 206
Db      484 ATGAATACTCTCCAAATGGCTTATAGATTGGGAAT-----GGTATTCCTTA 534
Qy      207 AlaAspIleMetGlyArgLysPheGlySerThrLysIleProTyrAsnProArgLysSer 226
Db      535 GCATCTATTATTTGGTAAAGATGGCGCATTCGTTGGAAA---GTTACCAAAAACCT 591
Qy      227 TrpAlaGlySerIleSerMetPheIlePheGlyPhePheIleSerIleAlaLeuLeuTyr 246
Db      592 TTAAAGGGAACCTTGGCTTTATAGTAAAGATTTCGTTTGTATGATATTTTACGT 651
Qy      247 TyrTyrSerSerLeuGlyTyrLeuHisMetAsnTrpLutTrpThrLeuGlnArgValAla 266
Db      652 TTGTATAAGCTGCATTTTAAACCACTTA-----ACTACTTTTCAATGTCTTACC 702
Qy      267 MetValSerMetValAlaThrValValGluSerLeuProIleThrAspGlnLeuAspAsp 286
Db      703 CTTTGTACACCT---AGTGAGTGTCTAGAGTAAAGTAAATAGTGTG-----CTTAAATGAC 750
Qy      287 AsnIleSerValPro 291
Db      751 AATATTTTGAATACCT 765

RESULT 11
US-10-932-182A-1952
; Sequence 1952, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1952
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-1952

Alignment Scores:
Pred. No.: 6,95e-05 Length: 1560
Score: 143.50 Matches: 56
Percent Similarity: 46.2% Conservative: 48
Best Local Similarity: 24.9% Mismatches: 78
Query Match: 9.3% Indels: 43
DB: 7 Gaps: 9
US-10-634-548-2 (1-304) x US-10-932-182A-1952 (1-1560)

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Qy      84 LeuValIleSerPheGluSer---LeuThrLysArgAsnValIleGlnGlnSerLeuSer 102
Db      925 CTACGCTATCCGTAACAAGTATTTGATGTCGAAAGGACGTATGCTTAAATCCTCC 984
Qy      103 ArgLysLeuValHisIleLeuSerGlyLeuLeuPheValIleAlaTrpProIlePheSer 122
Db      985 CGAAGAGTGTGGCACTTATATATCTTACTTATAGTCCATCATCTCAAAATGATTTCA 1044
Qy      123 GlycerThrgluAlaArgTyrPheAlaAlaPheValProLeuValAsnGlyLeuArgLeu 142
Db      1045 -----AATTGTGAAATAAT 1059
Qy      143 ValIleAsnGlyLeu-----SerIle 149
Db      1060 GCATTGCTGGAACAATACCAAGCTTCTTATACGTTGAATATATAGTTTCAAAACCTTA 1119
Qy      150 SerProAsnSerMetLeuIleLysSerValThrArgGluGlyArgAlaGluGlyLeuLeu 169
Db      1120 CCGCTCTAGAGTCTCTTATTTGAAGTACAACTTGAAGAGTTTCCGAGCCAGAACCAT 1179
Qy      170 LysGlyProLeuPheTyr---ValLeuAlaLeuLeuPhe-----SerAlaValPhePhe 186
Db      1180 AGTGGGCCCTGATCATATCTTATCTTATTTATTTATTTGAAATATGATGATGATGTTG 1239
Qy      187 TrpArgGluSerProIleGlyMetIleSerLeuAlaMetMetCysGlyValAspGlyIle 206
Db      1240 GTGAATGACTGCCCATGGATTAATAGTTTGGGAAT-----GGGGAATCTGTG 1290
Qy      207 AlaAspIleMetGlyArgLysPheGlySerThrLysIleProTyrAsnProArgLysSer 226
Db      1291 GCATCTATTATCGGTAAAGATATGTCATAATGTGTTG---CGAGTACCCAAAGACT 1347
Qy      227 TrpAlaGlySerIleSerMetPheIlePheGlyPhePheIleSerIleAlaLeuLeuTyr 246
Db      1348 ATGAAGGGAACCTTGGCTTACCACTTAAGTTTATTTGTTGTGTGATTTACTTTAC 1407
Qy      247 TyrTyrSerSerLeuGlyTyrLeuHisMetAsnTrpLutTrpThrLeuGlnArgValAla 266
Db      1408 TTGTATAAGCAACCGTGTTCAGTCACTTA-----ACCGTTTTCAAATGTCTT 1455
Qy      267 MetValSerMetValAlaThrValValGluSerLeuProIleThrAspGlnLeuAspAsp 286
Db      1456 TGTGTTGTACATTTAAGCGGGTATTTGGAAGAAATAGTGTG-----CTAATATGAT 1506
Qy      287 AsnIleSerValPro 291
Db      1507 AATATTTTGAATACCT 1521

RESULT 12
US-10-932-182A-1952
; Sequence 1952, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1952
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-1952

Alignment Scores:
Pred. No.: 6,95e-05 Length: 1560

```



```

Db 3995 GGTATGTCGCCGAAAAGATATGCTGACGTGATATGCGCTTATCGGCAATTATTTGACT 4054
Qy MetGlyArgLysPheGlySerThrIlePro---TyrAspProArgLysSerThr--- 227
Db 4055 CTGCACGCTTTAGCATGTCACGTGACAGCCCTTCAGACCCATCAGCTGATTAACGAGCA 4114
Qy 228 AlaGlySerIle-----SerMetPheIlePheGlyPhePheIleSerIle 242
Db 4115 TCCGATCATCAGCAAAATGTTACTAATGAAATGGCTATCGCTTCTGACCGTCACTTTT 4174
Qy 243 AlaIleuLeuTyrTyrTyrSerSerLeuGlyTyrLeuHisMetAsnTrpGluThrThrIleu 262
Db 4175 GCACACTACTT-----TTTGCAGCTTTG-----ATTTCAGCCCTTTG----- 4210
Qy 263 GluArgValAlaMetValSerMetValAlaThrValAlaGluSerLeuProIleuThrAsp 282
Db 4211 -----CTCGCCTTATGCGCTTACACGCGCGACGACGACATCCCTCGTTAAATTA 4264
Qy 283 Glu-----LeuAspAspAsnIleSerValProIleuAlaThrIle 295
Db 4265 AAACAGGTTCCGTGAGTTTAATTTATTTAGTGCCTTATTAACGCACTACGCACTTGG 4324
Qy 296 LeuAlaAlaTyrLeuSerPhe 302
Db 4325 GTTATCGGTCGCTTAAGTTTT 4345

RESULT 14
US-10-793-626-2167
; Sequence 2167, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STRAPHYLOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2167
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-2167

Alignment Scores:
Pred. No.: 2.82 Length: 1152
Score: 98.50 Matches: 70
Percent Similarity: 40.9% Conservative: 58
Best Local Similarity: 22.4% Mismatches: 115
Query Match: 6.4% Indels: 71
DB: 8 Gaps: 13

US-10-634-548-2 (1-304) x US-10-793-626-2167 (1-1152)
Qy 13 GluLeuCysArgPheGlyAsnAsnSerLeuThrHisArgPheCysSerProGlyPhe 32
Db 181 CAATTCAGGTTTAAATCAAGTACGCTGCAAAATATTCATTTGAACA----- 231
Qy 33 LeuIleSerSerProCysPheIleGlyLeuThrGlyMetGlySerAlaThrGluLeuArg 52
Db 232 ATCATTTGTAATCC-----TGGTTGACTGTTTAAAGTCAAGGCAATTTATTTTG 282
Qy 53 AlaArgArgSerLeuIleSerSerAlaValAlaThrAsnSerLeuLeuHisAspValGly 72
Db 283 ATTAACAATGTAATTTATTTAGTGTGAAAAAGST-----TTAGAAAAGCTTCT 336
Qy 73 AlaThrValAlaValIleuGlyGlyAlaTyrAlaLeuValIleuSerPheGluSerLeuThr 92

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Db 337 AAATATGATGAGCTCTATATTTATTTTAAATATGTTGAGACAAATCTTTAACT 396
Qy 93 LysArgAsnValIleGln-----GlnSerLeuSer 102
Db 397 TTAGAGAGGTGCTTTAGAGAGGTGACGTTATATCTGCAACCTCGAGTTGAAGATATGCT 456
Qy 103 ArgLysLeuValHisIleLeuSerGlyLeuLeuPheValLeuAlaTrpProIlePheSer 122
Db 457 -----ATTCAGAGTCTACTATTTGGCTTAGGACAAATCGTTTTCAG 498
Qy 123 -----GlySerThrGluAlaArgTyrPheAlaAlaPheValPro----- 135
Db 499 CTGTCCCTAGGTACACACCGAATGATTAATGACACTATGACCTTAATAAATATGACG 558
Qy 136 -----LeuValAsnGlyLeuAlaGlyLeuValIleAsnGly 146
Db 559 ATTAAGTCTTCAGCACTTTCATATGTCGTAATGATATTTAAATTTCTGTCTGTGCTGGA 618
Qy 147 LeuSerIleSerProAsnSerMetLeuIleLysSerValThrArgGluGlyArgAlaGlu 166
Db 619 TTAGCTATATTTCTCGCGCTTAAAAACATTTGTTACCAACCCCAAGAGGC----- 669
Qy 167 GluLeuLeuGlyGlyProLeuPheTyrValLeuAlaLeuLeuPheSerAlaValPhePhe 186
Db 670 -----CTGGCTTATTTATTAAGGTTTACCACTAGATTTAGCGGAATGAC-TTT 719
Qy 187 TrpArgGluSerProIleGlyMetIleSerLeuAlaMetCysGlyGlyAsp-GlyIle 206
Db 720 TGGTACATCTTTTACTTATATTTTATTTTACTTATTTTCTTATTTTGGGCACTTACCTTTC 779
Qy 206 AlaAspIleMetGlyArgLysPheGlySer---ThrIleProTyrAsnProArgLys 225
Db 780 TATATCATTTATTAAGTAAATATGATCTAATTTTACTTAATAAATGATATAGTAAAGACA 839
Qy 225 sSerTrpAla-----GlySerIleSerMetPheIlePheGlyPhePheIleSerIleAl 243
Db 840 AAAGTGCATTCATAGTACTAGTACTGATTTATC-----ATTAGATATCC 887
Qy 243 AlaLeuLeuTyrTyrSerSerLeuGlyTyrLeuHisMetAsnTrpGluThrThrIleu 263
Db 888 AGCAACATTAATCTTTAGTACTAGTACTGATTTGCGTTTGGC----- 930
Qy 263 ArgValAlaMetValSerMetValAlaThrValAlaGluSerLeuProIleThrAspGlu 283
Db 931 -----GCTGATCAGATATTTGATATATG-----GATTT 959
Qy 283 LeuAspAspAsnIleSerValProLeuAlaThrIle 295
Db 960 TATGTATCTAATATTTCTTATGACCATTAAGGGGCACTA 996

RESULT 15
US-10-793-626-3427/c
; Sequence 3427, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STRAPHYLOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3427
; LENGTH: 3108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3427

```


Alignment Scores:

Pred. No.:	10.1	Length:	3108
Score:	98.50	Matches:	70
Percent Similarity:	40.9%	Conservative:	58
Best Local Similarity:	22.4%	Mismatches:	115
Query Match:	6.4%	Indels:	71
DB:	8	Gaps:	13

US-10-634-548-2 (1-304) x US-10-793-626-3427 (1-3108)

Search completed: March 16, 2006, 23:57:14
 Job time : 440 secs

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QY      13  GlnLeuCysArgPheGlyAsnAsnSerLeuThrHisArgPheCysSerProGlyPhe 32
DB      3087  CAATCATGAGTTTAAATCAAGTACGCTGACAAATATTCAATTGAAACA----- 3037
QY      33  LeuIleSerSerProCysPheIleGlyLeuThrGlyMetGlySerAlaThrGlnLeuArg 52
DB      3036  ATCATTTAGTAATCCA-----TGGTTGACTGTTTATAGTCGAAGCAATATTATTG 2986
QY      53  AlaArgSerSerLeuIleSerSerAlaValAlaThrAsnSerLeuLeuHisArgValGly 72
DB      2985  ATACAAATGTAATTGTTATGTTAGTGTGAAAAAGCT-----TTGAAAAAGCTTCT 2932
QY      73  AlaThrValAlaValLeuGlyValAlaThrAlaLeuValLeuSerPheGlnSerLeuThr 92
DB      2931  AAAATATATGATGCTCTATTATTATCTTTAAATTATGCTGTAGACAAATCTTTAACT 2872
QY      93  LysArgSerValIleGln-----GlnSerLeuSer 102
DB      2871  TTAGAAGTGCTTTAGAAAGTGTACGTTATATATCTGCAACCTCGAGTTGAAGATATGCT 2812
QY      103  ArgLysLeuValHisIleLeuSerGlyLeuLeuPheValLeuAlaTrpProIlePheSer 122
DB      2811  -----ATCAAGGTGACTATTTCCTTAGACAAATCGTTTTTACG 2770
QY      123  -----GlySerThrGlnAlaArgIlyrPheAlaAlaPheValPro----- 135
DB      2769  CTGTCCCTAGTACAAACCGAATGATTAATGACAGCTATGCACTTAATAATATATGACG 2710
QY      136  -----LeuValAsnGlyLeuArgLeuValIleAsnGly 146
DB      2709  ATAAAGCTTCAGCACTTTCATTTGCTGAATGAATATTTAATTTCTGTCTGGCTGGA 2650
QY      147  LeuSerIleSerProAsnSerMetLeuIleLysSerValThrArgGlnGlyArgAlaGln 166
DB      2649  TTAGCTATATTTCCTGCGCTTAAACATTTGGTTACCAACCCCAAGAAAGC----- 2599
QY      167  GlnLeuLeuLysGlyProLeuPheTyValLeuAlaLeuLeuPheSerAlaValPhePhe 186
DB      2598  -----CTGGCTTATTATTAAAGTTTACCACTAGTATTGCGCAAAATGAC-TTT 2549
QY      187  TrpArgGlnSerProIleGlyMetIleSerLeuAlaMetMetCysGlyGlyAsp-GlyrI 206
DB      2548  TGGTACATCTTTTACTTATTATTATTACTATTATTCTTATTGCGGCATTAACGCTTTC 2489
QY      206  eAlaAspIleMetGlyArgLysPheGlySer--ThrLysIleProTyAsnProArgLys 225
DB      2488  TATATCATATTATAGATTAATATATATATTTACTTAATAATGATAATGATAAAGACA 2429
QY      225  sSerTrpAla-----GlySerIleSerMetPheIlePheGlyPhePheIleSerIleAl 243
DB      2428  AAAAGTGCATATCATAGTATGTTACTGTTATTTATC-----ATTAGTATCCC 2381
QY      243  AlaLeuLeuTyTyTySerSerSerLeuGlyTyrLeuHisMetAsnTrpGlnThrThrLeuG 263
DB      2380  AGCAACATTATCTTTTATAGTCAATTCATTCGCTTTGCG----- 2338
QY      263  nArgValAlaMetValSerMetValAlaThrValValGlnSerLeuProIleThrAspG 283
DB      2337  -----GCTGTACGATATTGATAATATG-----GATTT 2309
QY      283  nLeuAspAspAsnIleSerValProLeuAlaThrIle 295
DB      2308  TATTGTATCTAATATATTCTTATGCAATTAGGGGACACTA 2272

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